

From: Whiteman, Brian
 Sent: Monday, April 10, 2006 11:26 AM
 To: STIC-Biotech/ChemLib
 Subject: seq search

09816688 High et al.

SEQ ID NO: 1

- 1) commercial database
- 2) us patents and published us patent applications

Please limit search to 20 amino acids or less

Thank you,

Brian Whiteman
 Remsen, 2D14
 mail box 2C18
 Patent Examiner - Art Unit 1635
 United States Patent and Trademark Office
 (571) 272-0764

SEARCHED
 INDEXED
 SERIALIZED
 FILED
 (STIC)

Point of Contact:
 Alexandra Waclawiw
 Technical Info. Specialist

 Searcher: _____
 Searcher Phone: _____ 4413
 Date Searcher Picked up: _____ 4/13
 Date completed: _____ 4/17
 Searcher Prep Time: _____ 10
 Online Time: _____ 11

 Type of Search
 NA# _____ AA#: \
 S/L: _____ Oligomer: _____
 Encode/Transl: _____
 Structure #: _____ Text: _____
 Inventor: _____ Litigation: _____

 Vendors and cost where applicable
 STN: _____ 126
 DIALOG: _____
 QUESTEL/ORBIT: _____
 LEXIS/NEXIS: _____
 SEQUENCE SYSTEM: _____
 WWW/Internet: _____
 Other (Specify): _____

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OM protein - protein search, using SW model

Run on: April 13, 2006, 08:49:59 ; Search time 163 Seconds

15.380 Million cell updates/sec
(without alignments)

Title: US-09-816-6888B-1

Perfect score: 30 Gapext 0.5
Sequence: 1 RKKRRK 6

Scoring table: BLOSUM62 Gapext 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 389445

Post-processing: Minimum Match 0% Maximum Match 100%
Listing First 150 summaries

Minimum DB seq length: 0 Maximum DB seq length: 21

Post-processing: Minimum Match 0% Maximum Match 100%
Listing First 150 summaries

Published Applications AA_Main: *
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2: /cgn2_6/_picodata/1/_pubpaa/US08_PUBCOMB.pep: *
3: /cgn2_6/_picodata/1/_pubpaa/US09_PUBCOMB.pep: *
4: /cgn2_6/_picodata/1/_pubpaa/US10_PUBCOMB.pep: *
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6: /cgn2_6/_picodata/1/_pubpaa/US11_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	30	100.0	6	4	US-10-445-235-5		Sequence 5, Appli
2	30	100.0	6	4	US-10-712-331-5		Sequence 5, Appli
3	30	100.0	9	3	US-09-816-688A-1		Sequence 1, Appli
4	27	100.0	15	9	US-10-912-764-45		Sequence 45, Appli
5	27	90.0	8	3	US-09-876-904A-348		Sequence 348, Appli
6	27	90.0	8	4	US-10-028-056-25		Sequence 25, Appli
7	27	90.0	8	4	US-10-211-088-230		Sequence 230, Appli
8	27	90.0	8	5	US-10-482-029-359		Sequence 359, Appli
9	27	90.0	12	3	US-09-933-780C-35		Sequence 35, Appli
10	27	90.0	13	3	US-09-170-70-39		Sequence 39, Appli
11	27	90.0	19	4	US-10-025-567A-1183		Sequence 1183, Appli
12	27	90.0	21	3	US-09-844-761-48960		Sequence 48960, A
13	26	86.7	8	4	US-10-057-620-7		Sequence 7, Appli
14	26	86.7	10	5	US-10-902-029-49		Sequence 49, Appli
15	26	86.7	10	5	US-10-983-169-2		Sequence 2, Appli
16	26	86.7	11	5	US-10-983-163-11		Sequence 11, Appli
17	26	86.7	13	5	US-09-746-170-26		Sequence 26, Appli
18	26	86.7	13	3	US-09-746-170-31		Sequence 31, Appli
19	26	86.7	13	3	US-09-746-170-35		Sequence 49, Appli
20	26	86.7	10	5	US-10-983-163-37		Sequence 2, Appli
21	26	86.7	15	5	US-10-983-163-3		Sequence 3, Appli
22	26	86.7	19	5	US-10-983-163-10		Sequence 10, Appli
23	25	83.3	6	3	US-09-809-790-7		Sequence 7, Appli
24	25	83.3	6	3	US-09-809-790-8		Sequence 8, Appli
25	25	83.3	6	3	US-09-809-617-7		Sequence 7, Appli
26	25	83.3	6	3	US-09-809-617-8		Sequence 8, Appli
27	25	83.3	8	3	US-09-876-904A-360		Sequence 360, Appli

Result No.	Score	Query	Match	Length	DB	ID	Description
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30	83.3	31	83.3	13	3	US-09-746-170-17	Sequence 17, Appli
31	83.3	25	83.3	13	3	US-09-746-170-28	Sequence 28, Appli
32	83.3	25	83.3	13	4	US-10-776-121A-88	Sequence 33, Appli
33	83.3	25	83.3	13	5	US-10-660-370-305	Sequence 88, Appli
34	83.3	25	83.3	13	5	US-09-976-904A-212	Sequence 305, Appli
35	83.3	35	83.3	15	3	US-10-976-904A-370	Sequence 372, Appli
36	83.3	25	83.3	20	5	US-10-978-112A-2	Sequence 2, Appli
37	83.3	37	83.3	20	5	US-10-978-112A-3	Sequence 10, Appli
38	83.3	39	83.3	20	5	US-10-978-112A-4	Sequence 4, Appli
39	83.3	40	83.3	20	5	US-10-978-112A-8	Sequence 8, Appli
40	83.3	41	83.3	20	5	US-10-978-112A-9	Sequence 9, Appli
41	83.3	42	83.3	20	5	US-10-978-112A-10	Sequence 10, Appli
42	83.3	43	83.3	21	4	US-10-916-481-8	Sequence 8, Appli
43	83.3	44	83.3	21	4	US-10-311-088-241	Sequence 241, Appli
44	83.3	45	83.3	21	4	US-10-323-157-8	Sequence 8, Appli
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49	83.3	50	83.3	21	5	US-10-151-724-8	Sequence 2, Appli
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51	80.0	52	80.0	6	3	US-09-992-480-2	Sequence 2, Appli
52	80.0	53	80.0	6	3	US-09-947-946A-149	Sequence 149, Appli
53	80.0	54	80.0	6	3	US-09-906-311C-145	Sequence 14, Appli
54	80.0	55	80.0	6	3	US-10-983-960-2	Sequence 2, Appli
55	80.0	56	80.0	6	4	US-10-309-421-3	Sequence 2, Appli
56	80.0	57	80.0	6	4	US-10-229-915-33	Sequence 33, Appli
57	80.0	58	80.0	6	4	US-10-366-433-88	Sequence 88, Appli
58	80.0	59	80.0	6	4	US-10-338-348-5	Sequence 5, Appli
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61	80.0	62	80.0	6	4	US-10-366-433-88	Sequence 6, Appli
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69	80.0	70	80.0	7	3	US-09-792-480-32	Sequence 32, Appli
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72	80.0	73	80.0	7	3	US-09-847-946A-150	Sequence 156, Appli
73	80.0	74	80.0	7	3	US-09-746-156-156	Sequence 27, Appli
74	80.0	75	80.0	7	3	US-09-006-311C-27	Sequence 52, Appli
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84	80.0	85	80.0	7	4	US-10-209-421-24	Sequence 26, Appli
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92	80.0	93	80.0	7	4	US-10-121-38-38	Sequence 37, Appli
93	80.0	94	80.0	7	4	US-10-229-915-34	Sequence 34, Appli
94	80.0	95	80.0	7	4	US-10-338-348-6	Sequence 6, Appli
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96	80.0	97	80.0	7	4	US-10-972-963-6	Sequence 4, Appli
97	80.0	98	80.0	7	4	US-10-778-175B-44	Sequence 44, Appli
98	80.0	99	80.0	8	3	US-10-992-180-4	Sequence 4, Appli
99	80.0	100	80.0	8	3	US-09-876-904A-360	Sequence 26, Appli

RESULT 1
 US-10-445-235-5
 Sequence 5, Application US-10445235
 Publication No. US20040005670A1
 GENERAL INFORMATION:
 APPLICANT: Katherine A. High
 FILE REFERENCE: CHOP176
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF HEMOPHILIA A
 CURRENT FILING DATE: 2003-05-22
 PRIOR APPLICATION NUMBER: US-10/445,235
 PRIORITY FILING DATE: 2002-05-22
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 5 LENGTH: 6

RESULT 2
 US-10-712-332-5
 Sequence 5, Application US-10712332
 Publication No. US2004007257A1
 GENERAL INFORMATION:
 APPLICANT: Wolf, David L.
 TITLE OF INVENTION: Agents Affecting Thrombosis and Hemostasis
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morgan, Lewis & Bockius LLP
 STREET: 111 Pennsylvania Avenue, NW
 CITY: Washington
 STATE: DC
 COUNTRY: ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-10/712,332
 FILING DATE: 13-Nov-2003
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US-09/671,346
 FILING DATE: 27-Sep-2000
 APPLICATION NUMBER: US-07/578,646
 FILING DATE: 1990-09-04
 APPLICATION NUMBER: US-07/806,329
 FILING DATE: 1991-12-16
 APPLICATION NUMBER: US-08/249,777
 FILING DATE: 1994-05-26
 APPLICATION NUMBER: US-08/268,003
 FILING DATE: 1994-06-29
 APPLICATION NUMBER: US-08/469,301
 FILING DATE: 1995-06-06
 APPLICATION NUMBER: US-09/016,403
 FILING DATE: 1998-01-30
 APPLICATION NUMBER: US-09/362,207
 FILING DATE: 1999-07-28
 ATTORNEY/AGENT INFORMATION:
 NAME: Michael S. Tuscan, Ph.D.
 REGISTRATION NUMBER: 43,210
 REFERENCE/DOCKET NUMBER: 44481-5002-15-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 739-3000
 TELEFAX: (202) 739-3001
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 ; US-10-712-332-5
 Query Match 100.0% Score 30; DB 4; Length 6;

RESULT 1
 US-10-445-235-5
 Sequence 5, Application US-10445235
 Publication No. US20040005670A1
 GENERAL INFORMATION:
 APPLICANT: Rodney M. Camire
 FILE REFERENCE: CHOP176
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF HEMOPHILIA A
 CURRENT FILING DATE: 2003-05-22
 PRIOR APPLICATION NUMBER: US-10/445,235
 PRIORITY FILING DATE: 2002-05-22
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 5 LENGTH: 6

RESULT 2
 US-10-712-332-5
 Sequence 5, Application US-10712332
 Publication No. US2004007257A1
 GENERAL INFORMATION:
 APPLICANT: Wolf, David L.
 TITLE OF INVENTION: Agents Affecting Thrombosis and Hemostasis
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morgan, Lewis & Bockius LLP
 STREET: 111 Pennsylvania Avenue, NW
 CITY: Washington
 STATE: DC
 COUNTRY: ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-10/712,332
 FILING DATE: 13-Nov-2003
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US-09/671,346
 FILING DATE: 27-Sep-2000
 APPLICATION NUMBER: US-07/578,646
 FILING DATE: 1990-09-04
 APPLICATION NUMBER: US-07/806,329
 FILING DATE: 1991-12-16
 APPLICATION NUMBER: US-08/249,777
 FILING DATE: 1994-05-26
 APPLICATION NUMBER: US-08/268,003
 FILING DATE: 1994-06-29
 APPLICATION NUMBER: US-08/469,301
 FILING DATE: 1995-06-06
 APPLICATION NUMBER: US-09/016,403
 FILING DATE: 1998-01-30
 APPLICATION NUMBER: US-09/362,207
 FILING DATE: 1999-07-28
 ATTORNEY/AGENT INFORMATION:
 NAME: Michael S. Tuscan, Ph.D.
 REGISTRATION NUMBER: 43,210
 REFERENCE/DOCKET NUMBER: 44481-5002-15-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 739-3000
 TELEFAX: (202) 739-3001
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 ; US-10-712-332-5
 Query Match 100.0% Score 30; DB 4; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0; Db 5 RKRKKR 10

Qy 1 RKRKKR 6
Db 1 RKRKKR 6

RESULT 3

US-09-816-688A-1 Application US/09816688A
; Sequence 1, Application US/09816688A
; Publication No. US20040102388A1
; GENERAL INFORMATION:
; APPLICANT: THE CHILDREN'S HOSPITAL OF PHILADELPHIA
; APPLICANT: HIGH, KATHERINE
; APPLICANT: MARGARITAS, PARIS
; APPLICANT: CAMTRIE, RODNEY
; TITLE OF INVENTION: MODIFIED BLOOD CLOTTING FACTORS AND METHODS OF USE
; FILE REFERENCE: 018743-0278737
; CURRENT APPLICATION NUMBER: US/09/816,688A
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/191,331
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic proteolytic cleavage
; OTHER INFORMATION: peptide
us-09-816-688A-1

Qy 1 RKRKKR 6
Db 1 RKRKKR 6

Query Match 100.0%; Score 30; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6

US-10-028-056-25 Application US/10028056
; Sequence 25, Application US/10028056
; Publication No. US2002152483A1
; GENERAL INFORMATION:
; APPLICANT: REUE, KAREN
; APPLICANT: PTERFY, MIKLOS
; TITLE OF INVENTION: A NOVEL GENE ASSOCIATED WITH REGULATION OF ADIPOSITY AND INSULIN F
; FILE REFERENCE: 4077-8980100US
; CURRENT APPLICATION NUMBER: US/10/028,056
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 60/257,772
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO: 25
; SOFTWARE: PatentIn version 3.0
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
us-10-028-056-25

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Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRKKR 6
Db 1 RKRKKR 6

RESULT 7

US-10-211-088-230 Application US/10211088
; Sequence 230, Application US/10211088
; Publication No. US2003104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.

Qy 1 RKRKKR 6
Db 1 RKRKKR 6

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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.2
SEQ ID NO: 35
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-933-780C-35

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Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRKR 6
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Db 2 RKRKR 7

RESULT 10
US-09-746-170-39
; Sequence 39, Application US/09746170
; Publication No. US200217543A1
; GENERAL INFORMATION:
; APPLICANT: Karr, Jonathan
; APPLICANT: Walker, Stephen
; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT APPLICATION NUMBER: US/09/746,170
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60,171,804
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin version 3.0
SEQ ID NO 39
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-746-170-39

Query Match 90.0%; Score 27; DB 3; Length 13;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRKR 6
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Db 2 RKRKR 7

RESULT 11
US-10-225-567A-1183
; Sequence 1183, Application US/10225567A
; Publication No. US200313798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 19204-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60,257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2392
; SOFTWARE: Patentin version 3.1
SEQ ID NO 1183
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1183

Query Match 90.0%; Score 27; DB 3; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRKR 6
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Db 2 RKRKR 7

RESULT 9
US-09-933-780C-35
; Sequence 35, Application US/09933780C
; Publication No. US200322922A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMACEUTICALS INC.
; APPLICANT: GUO, Yong
; APPLICANT: MORSE, Clarence C
; APPLICANT: YAO, Zhengbin
; TITLE OF INVENTION: MEMBRANE PENETRATING PEPTIDES AND USES THEREOF
; FILE REFERENCE: HMR2053 PCT
; CURRENT APPLICATION NUMBER: US/09/933,780C
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,647
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: GB 0103110.3
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: GB 0103110.3
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.2
SEQ ID NO: 35
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-933-780C-35

Query Match 90.0%; Score 27; DB 4; Length 19;

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RESULT 15
US-10-983-169-2
; Sequence 2, Application US/10983169
; Publication No. US20050196383A1
; GENERAL INFORMATION:
; APPLICANT: Zurbriggen, Rinaldo E.
; TITLE OF INVENTION: Compositions and Methods for the Potentiation of Immune Responses
; FILE REFERENCE: 126442-1-00012
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US/10/983,169
; CURRENT FILING DATE: 2004-11-05
; PRIOR FILING DATE: 2003-11-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 2
; LENGTH: 10
; TYPE: PRT
; FEATURE:
; OTHER INFORMATION: Synthetic peptide derived from Apis mellifera
; US-10-983-169-2

US-09-746-170-31
; Query Match Score 26; DB 5; Length 10;
; Best Local Similarity 83.3%; Pred. No. 4.1e+02;
; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RKRKR 6
Db 2 RKRQKR 7

RESULT 16
US-10-983-169-11
; Sequence 11, Application US/10983169
; Publication No. US20050196383A1
; GENERAL INFORMATION:
; APPLICANT: Zurbriggen, Rinaldo E.
; TITLE OF INVENTION: Compositions and Methods for the Potentiation of Immune Responses
; FILE REFERENCE: 126442-1-00012
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US/10/983,169
; CURRENT FILING DATE: 2004-11-05
; PRIOR FILING DATE: 2003-11-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 11
; LENGTH: 11
; TYPE: PRT
; FEATURE:
; OTHER INFORMATION: Cys-Me1
; US-10-983-169-11

US-09-746-170-31
; Query Match Score 26; DB 5; Length 11;
; Best Local Similarity 83.3%; Pred. No. 4.5e+02;
; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RKRKR 6
Db 3 RKRQKR 8

RESULT 17
US-09-746-170-26
; Sequence 26, Application US/09746170
; Patent No. US2002127543A1
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; APPLICANT: Walker, Stephen
; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/746,170
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO: 35
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; US-09-746-170-35

US-09-746-170-31
; Query Match Score 26; DB 3; Length 13;
; Best Local Similarity 83.3%; Pred. No. 5.2e+02;
; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RKRKR 6
Db 2 RKRQKR 7

RESULT 18
US-09-746-170-31
; Sequence 31, Application US/09746170
; Patent No. US2002127543A1
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; APPLICANT: Walker, Stephen
; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,804
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 31
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; US-09-746-170-31

US-09-746-170-31
; Query Match Score 26; DB 3; Length 13;
; Best Local Similarity 83.3%; Pred. No. 5.2e+02;
; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RKRKR 6
Db 2 RKRQKR 7

RESULT 19
US-09-746-170-35
; Sequence 35, Application US/09746170
; Patent No. US2002127543A1
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; APPLICANT: Walker, Stephen
; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,804
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 35
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; US-09-746-170-35

```

Query Match Similarity 86.7%; Score 26; DB 3; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5.2e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0;
 SEQ ID NO: 37

Db 1 RKRKR 6
 1 |||:
 2 RKRKRQ 7

RESULT 20
 US-09-746-170-37
 ; Sequence 37, Application US/09746170
 ; GENERAL INFORMATION:
 ; APPLICANT: Karn, Jonathan
 ; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
 ; FILE REFERENCE: 2262/01280
 ; CURRENT APPLICATION NUMBER: US/09/746,170
 ; CURRENT FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/171,804
 ; PRIOR FILING DATE: 1999-12-22
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 37
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Hepatitis C virus

US-09-746-170-37

Query Match Similarity 86.7%; Score 26; DB 3; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5.2e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0;

SEQ ID NO: 37

RESULT 21
 US-10-983-169-3
 ; Sequence 3, Application US/10983169
 ; GENERAL INFORMATION:
 ; APPLICANT: Zurbriggen, Rinaldo E.
 ; TITLE OF INVENTION: Compositions and Methods for the Potentiation of Immune Responses
 ; FILE REFERENCE: 126442-10012
 ; CURRENT APPLICATION NUMBER: US/10/983,169
 ; CURRENT FILING DATE: 2004-11-05
 ; PRIOR APPLICATION NUMBER: US 60/517,502
 ; PRIOR FILING DATE: 2003-11-05
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 3
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; OTHER INFORMATION: Synthetic peptide derived from *Apis mellifera*

US-10-983-169-3

Qy 1 RKRKR 6
 1 |||:
 2 RKRKRQ 7

Query Match Similarity 86.7%; Score 26; DB 5; Length 15;
 Best Local Similarity 83.3%; Pred. No. 5.8e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0;

RESULT 24
 US-09-809-790-8
 ; Sequence 8, Application US/09809790
 ; Patent No. US20020072102A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheppard, Paul O.
 ; TITLE OF INVENTION: FastSEQ for Windows Version 3.0
 ; FILE REFERENCE: 98-29
 ; CURRENT APPLICATION NUMBER: US/09/809,790
 ; CURRENT FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 09/351,414
 ; PRIOR FILING DATE: 1999-07-09
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 7
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: antigenic peptide

US-09-809-790-7

Qy 2 KBRKR 6
 2 |||:
 1 KBRKR 5

Query Match Similarity 83.3%; Score 25; DB 3; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

RESULT 22
 ; Sequence 22, Application US/09809790
 ; Patent No. US20020072102A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baindur, Nand
 ; TITLE OF INVENTION: Deisher, Theresa A.

```

; PRIOR APPLICATION NUMBER: US/09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
; US-09-809-617-8

Query Match 83.3%; Score 25; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRRKR 6
Db 2 KRRKR 6

RESULT 25
US-09-809-617-7
; Sequence 7, Application US/09809617
; Patent No. US2002137178A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baindur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,617
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US/09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
; US-09-809-617-7

Query Match 83.3%; Score 25; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRRKR 6
Db 1 KRRKR 5

RESULT 26
US-09-809-617-8
; Sequence 8, Application US/09809617
; Patent No. US2002137178A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baindur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/351,414
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US/09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 194
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
; US-09-809-617-8

Query Match 83.3%; Score 25; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRRKR 6
Db 1 KRRKR 5

RESULT 28
US-10-660-370-194
; Sequence 194, Application US/10660370
; Publication No. US20050004507A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, J. Stephen
; APPLICANT: National Institutes of Health
; TITLE OF INVENTION: Determining Kinase Specificity
; FILE REFERENCE: 1662-0050US2
; CURRENT APPLICATION NUMBER: US/10/660,370
; CURRENT FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 640
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 194
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
; US-10-660-370-194

Query Match 83.3%; Score 25; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRRKR 5
Db 2 KRRKR 6

```

; OTHER INFORMATION: A synthetic peptide
us-10-660-370-194

Query Match 83.3%; Score 25; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 7e+02; Indels 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Qy 2 KRRKR 6
Db 1 KRRKR 5

RESULT 29

us-09-746-170-8
; Sequence 8, Application US/09746170
; Patent No. US20020127542A1
; GENERAL INFORMATION:
; APPLICANT: Kurn, Jonathan
; APPLICANT: Walker, Stephen
; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT APPLICATION NUMBER: US/09/746,170
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,804
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
us-09-746-170-8

Query Match 83.3%; Score 25; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.5e+02; Indels 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 RGRRK 5
Db 6 RGRRK 10

RESULT 30

us-09-746-170-17
; Sequence 17, Application US/09746170
; Patent No. US20020127542A1
; GENERAL INFORMATION:
; APPLICANT: Kurn, Jonathan
; APPLICANT: Walker, Stephen
; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT APPLICATION NUMBER: US/09/746,170
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,804
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
us-09-746-170-17

Query Match 83.3%; Score 25; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.5e+02; Indels 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 RGRRK 5
Db 6 RGRRK 10

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Result No.	Score	Query Match	Length	DB ID	Description
1	3.0	100.0	6	4 AAU09934	Aau09934 Synthetic Adf09125 PACE-furi
2	3.0	100.0	6	8 ADP09125	Adk08902 Human pap
3	3.0	100.0	8	8 ADP08902	Aar42225 Anti-herp
4	3.0	100.0	9	2 AAF70502	Aar70502 Anti-cyto
5	3.0	100.0	9	2 AAF70502	Aaw24810 Anti-cyto
6	3.0	100.0	9	2 AAW24810	Aaw24809 Anti-cyto
7	3.0	100.0	9	2 AAW24810	Aaw24811 Anti-cyto
8	3.0	100.0	9	6 ABR07953	Abr07953 Human can
9	3.0	100.0	9	6 ABR08153	Abr08153 Human can
10	3.0	100.0	6	6 ABR08701	Abr08701 Human can
11	3.0	100.0	9	6 ABR07954	Abr07954 Human can
12	3.0	100.0	9	6 ABR08474	Abr08474 Human can
13	3.0	100.0	9	6 ABR08536	Abr08536 Human can
14	3.0	100.0	9	6 ABR08558	Abr08558 Human can
15	3.0	100.0	9	6 ABR08701	Abr08701 Human can
16	3.0	100.0	9	6 ABR07558	Abr07558 Human can
17	3.0	100.0	9	6 ABR08154	Abr08154 Human can
18	3.0	100.0	9	8 ADP08956	Adk08966 Human pap
19	3.0	100.0	10	6 ABR08921	Abr08921 Human can
20	3.0	100.0	10	6 ABR08402	Abr08402 Human can
21	3.0	100.0	10	6 ABR08569	Abr08569 Human can
22	3.0	100.0	10	6 ABR08053	Abr08053 Human can
23	3.0	100.0	10	6 ABR08455	Abr08455 Human can
24	3.0	100.0	10	6 ABR08599	Abr08599 Human can

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3.0	100.0	6	4 AAU09934	Aau09934 Synthetic Adf09125 PACE-furi
2	3.0	100.0	6	8 ADP09125	Adk08902 Human pap
3	3.0	100.0	8	8 ADP08902	Aar42225 Anti-herp
4	3.0	100.0	9	2 AAF70502	Aar70502 Anti-cyto
5	3.0	100.0	9	2 AAF70502	Aaw24810 Anti-cyto
6	3.0	100.0	9	2 AAW24810	Aaw24809 Anti-cyto
7	3.0	100.0	9	2 AAW24810	Aaw24811 Anti-cyto
8	3.0	100.0	9	6 ABR07953	Abr07953 Human can
9	3.0	100.0	9	6 ABR08153	Abr08153 Human can
10	3.0	100.0	6	6 ABR08701	Abr08701 Human can
11	3.0	100.0	9	6 ABR07954	Abr07954 Human can
12	3.0	100.0	9	6 ABR08474	Abr08474 Human can
13	3.0	100.0	9	6 ABR08536	Abr08536 Human can
14	3.0	100.0	9	6 ABR08558	Abr08558 Human can
15	3.0	100.0	9	6 ABR08701	Abr08701 Human can
16	3.0	100.0	9	6 ABR07558	Abr07558 Human can
17	3.0	100.0	9	6 ABR08154	Abr08154 Human can
18	3.0	100.0	9	8 ADP08956	Adk08966 Human pap
19	3.0	100.0	10	6 ABR08921	Abr08921 Human can
20	3.0	100.0	10	6 ABR08402	Abr08402 Human can
21	3.0	100.0	10	6 ABR08569	Abr08569 Human can
22	3.0	100.0	10	6 ABR08053	Abr08053 Human can
23	3.0	100.0	10	6 ABR08455	Abr08455 Human can
24	3.0	100.0	10	6 ABR08599	Abr08599 Human can

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

98	21	4	ABB32457	Peptide #	KW	Bernard-Soulier's thrombasthenia; decreased clotting time.
99	27	90.0	ABB31280	Nuclear 1	XX	
100	26	86.7	ABB31280	Human fac	OS	Synthetic.
101	26	86.7	AAAG86555	Saccharom	XX	
102	26	86.7	AD225756	Peptide d	XX	
103	26	86.7	ABR47550	Peptide d	XX	
104	26	86.7	ABR30411	Nuclear 1	XX	
105	26	86.7	ABR47559	Peptide c	XX	
106	26	86.7	AAV69769	RNA bindi	PP	22-MAR-2001; 2001WO-US009355.
107	26	86.7	AAV69765	RNA bindi	XX	
108	26	86.7	AAV69771	RNA bindi	PR	22-MAR-2000; 2000US-0191331P.
109	26	86.7	AAV69760	RNA bindi	XX	
110	26	86.7	AAU06106	RNA bindi	PA	(CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
111	26	86.7	AAU06097	RNA bindi	XX	
112	26	86.7	AAU06108	RNA bindi	PI	High KA, Margaritis P, Camire RM;
113	26	86.7	AAU06102	RNA bindi	XX	
114	26	86.7	ADU15719	MUC1-PDZ	DR	WPI; Page 41; 55pp; English.
115	26	86.7	AAU061551	Peptide d	XX	
116	26	86.7	ABH11553	Apolipop	PT	Mutant blood clotting factors useful for treating a bleeding or clotting
117	26	86.7	ABR47558	Amino aci	PT	disorder in a subject, comprising a modified proteolytic cleavage site
118	25	83.3	AAW6219	Fusion pr	PT	not normally present in the factor.
119	25	83.3	AAE33758	Peptide u	XX	
120	25	83.3	AAV54459	Antigenic	PS	Claim 9; Page 41; 55pp; English.
121	25	83.3	AAV54458	Antigenic	XX	
122	25	83.3	AAU07191	Human dis	CC	The invention relates to a new composition comprising a recombinant
123	25	83.3	AAU07192	Human dis	CC	polynucleotide that encodes a modified blood clotting factor (MBCP),
124	25	83.3	ABb78131	Epitope b	CC	where the modification comprises a proteolytic cleavage site not normally
125	25	83.3	ABb78132	Epitope b	CC	present in the factor, and where the factor is cleaved at the cleavage
126	25	83.3	ABR41490	Kappa B/V	CC	site when expressed in an animal cell. The new composition is useful for
127	25	83.3	ABR41455	GAG-bindi	CC	treating a bleeding or clotting disorder of a subject, preferably mammal
128	25	83.3	ABR42006	GAG-bindi	CC	especially human, having or at risk of having such a disorder, amenable
129	25	83.3	ABR41454	GAG-bindi	CC	to treatment with Factor VII, Factor VIII or Factor IX and caused by
130	25	83.3	ABR41496	Kappa B/V	CC	insufficient activity of expression of a vitamin-K dependent
131	25	83.3	ABR42007	GAG-bindi	CC	procoagulant, or by insufficient platelet aggregation. The disorder
132	25	83.3	AYO5442	Bronchodi	CC	comprises haemophilia A or B, or Factor VII
133	25	83.3	ABW02277	Small nuc	CC	deficiency, Glanzmann's thrombasthenia or Bernard-Soulier's
134	25	83.3	ABB74596	Transcrip	CC	B thrombasthenia. The subject produces inhibitory antibodies that bind to a
135	25	83.3	ADK08903	Human pap	CC	clotting factor, preferably Factor VIII or Factor IX. The composition of
136	25	83.3	AAE24005	GAG-bindi	CC	the invention is also useful for decreasing clotting time and for
137	25	83.3	ABR41486	Kappa B/V	CC	reducing the frequency or severity of bleeding in a subject. Unlike wild
138	25	83.3	ABR05609	Peptide a	CC	type Factor VII, MBCP comprises a Factor VII having increased activity,
139	25	83.3	ABR07493	Ruman can	CC	immunogenicity in vivo; and the
140	25	83.3	ABR07871	Ruman can	CC	increased stability of the cleaved factor eliminates proteolytic cleavage during
141	25	83.3	ABR08071	Ruman can	CC	the blood clotting process. The present peptide sequence represents a
142	25	83.3	ADK08968	Human pap	CC	synthetic proteolytic cleavage recognition site of the invention
143	25	83.3	ADK08967	Human pap	XX	
144	25	83.3	ABR0637	Human can	SQ	Sequence 6 AA;
145	25	83.3	ABR07588	Human can	Query Match	100.0%; Score 30; DB 4; Length 6;
146	25	83.3	ABR08008	Human can	Best Local Similarity	100.0%; Pred. No. 2e+06;
147	25	83.3	ABR08183	Human can	Matches	6; Conservat 0; Mismatches 0;
148	25	83.3	ADK09035	Human pap	Indels	0; Gaps 0
149	25	83.3	ADK09034	Human pap		
150	25	83.3	ABR28129	Cell-to-c		

SCIENCE

RESULT 1
AAU09934 standard: ventricle: 6 AA
ID AAU09934

AAU090934;	AC	ADP09125;
18-JUN-2002 (first entry)	DT	26-FEB-2004 (first entry)
Synthetic proteolytic cleavage recognition site peptide sequence #1.	XX	XX
Proteolytic cleavage recognition site; haemostatic; factor VII-agonist; factor VIII-agonist; factor IX-agonist; modified blood clotting factor; MBCP; bleeding disorder; clotting disorder; Factor VII; Factor VIII; Factor IX; vitamin-K procoagulant; platelet aggregation; haemophilia; Glaenzmann's thrombasthenia; antibody; immunogenicity;	DE	PAGE-furin-like protease cleavage site peptide SEQ ID NO:5.
human; factor VIII; FVIII; variant; haemostatic; gene therapy; Synthetic.	XX	KW haemophilia.
XX	XX	OS
XX	XX	PN
		WO2003100053-A1.

XX	04-DEC-2003.	PT	New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
PD		PT	
XX		PT	
PP	22-MAY-2003; 2003WO-US016376.	XX	
PR	22-MAY-2002; 2002US-0382486P.	XX	
PR	(CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.	XX	
PI	High KA, Camire RM;	XX	
PI	WPI; 2004-035147/03.	XX	
XX	New nucleic acid sequence encoding a biologically active recombinant human factor VIII variant, useful for preparing a composition for treating hemophilia.	XX	
XX	Claim 3; SEQ ID NO 5; 57pp; English.	XX	
XX	The present invention describes an isolated nucleic acid sequence encoding a biologically active recombinant human factor VIII (FVIII) variant comprising variants set forth in table 2 in the specification (see page 32-33). Also described: (1) a vector comprising the nucleic acid sequence; (2) an isolated modified human FVIII protein produced by expression of the nucleic acid; and (3) a method of treating haemophilia in a patient. Human FVIII has haemostatic activity, and can be used in gene therapy. The nucleic acid can be used for preparing a composition for treating haemophilia. The present sequence represents a PACB-furin-like protease cleavage site peptide, which is used in the exemplification of the present invention. The human FVIII gene is located on chromosome X, more specifically to Xq28.	XX	
XX	Sequence 6 AA;	XX	
XX	Query Match 100.0%; Score 30; DB 8; Length 6;	XX	
CC	Best Local Similarity 100.0%; Pred. No. 2e+06;	XX	
CC	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	
Qy	1 RKRKRK 6	XX	
Db	1 RKRKRK 7	XX	
XX	RESULT 4	XX	
XX	AAR42225 standard; peptide; 9 AA.	XX	
XX	Sequence 8 AA;	XX	
XX	Query Match 100.0%; Score 30; DB 8; Length 8;	XX	
CC	Best Local Similarity 100.0%; Pred. No. 2e+06;	XX	
CC	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	
Qy	1 RKRKRK 6	XX	
Db	2 RKRKRK 7	XX	
XX	RESULT 4	XX	
XX	AAR42225 (revised)	XX	
XX	ID AAR42225;	XX	
XX	AC AAR42225;	XX	
XX	DT 25-MAR-2003 (revised)	XX	
XX	DT 17-MAY-1994 (first entry)	XX	
XX	PD 11-NOV-1993.	XX	
XX	PP 21-APR-1993;	XX	
XX	PR 23-APR-1992;	XX	
XX	PA (KIRW /) KIRWOOD S. D.	XX	
XX	PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.	XX	
XX	PI Twist M, Barnett RW, Summer-Smith M;	XX	
XX	DR WPI; 1993-368410/46.	XX	
XX	XX Compens. for treatment of herpes virus infections - contg. PT oligopeptide (s), esp. nona:D-arginine peptide, as active agent.	XX	
XX	XX Disclosure; Page 9; 36pp; English.	XX	
XX	XX The peptide may be used in a compen. for the treatment of herpes virus infection in humans or animals, this may be administered topically or systemically. The peptide is prep'd by conventional methods, e.g., by solid phase synthesis methods. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)	XX	
XX	Sequence 9 AA;	XX	
XX	Query Match 100.0%; Score 30; DB 2; Length 9;	XX	
XX	Best Local Similarity 100.0%; Pred. No. 2e+06;	XX	
XX	WPI; 2004-169243/16.	XX	

PP 14-DEC-1994; 94US-00357056.
 XX 24-OCT-1990; 90US-00602953.
 PR 23-OCT-1991; 91US-00779135.
 XX (ALLIX) ALLELIX BIOPHARMACEUTICALS INC.
 XX Sonenberg N, Reid LS, Barnett RW, Summer-Smith M;
 PI DR WPI; 1997-362969/33.
 XX New D-arginine oligomers - useful as antiviral agents, especially against
 HIV.
 XX Disclosure; Col 6; 14PP; English.
 XX The sequences given in AAW2605-33 represent peptides which can be used
 CC in D-Arginine Oligomers of formula: R1-X-R2 (I). R1 = H, lower alkanoyl,
 CC a deaminated amino acid or N-terminal protecting group; R2 = OH, lower
 CC alkyl, amino, mono- or di(lower alkyl) amino, a decarboxylated amino acid
 CC or a C-terminal protecting group; X = a chain of 7-12 D-arginine
 CC residues. The compounds are useful as antiviral agents, especially for
 CC inhibiting HIV replication. They are administered in intravenous doses of
 CC 1 microg/kg to 10 mg/kg, especially 0.1-5 mg/kg. (Updated on 25-MAR-2003
 CC to correct PP field.)
 XX Sequence 9 AA;
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ7120-ABZ78168 and ABR01861). The genes and
 CC proteins are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX Sequence 9 AA;
 SQ Query Match 100 0%; Score 30; DB 6; Length 9;
 CC Best Local Similarity 100 0%; Pred. No. 2e+06;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AC ABR0153;
 CC Human cancer-related protein 151PIC7A HLA peptide #688.
 CC Human; cytostatic; vaccine; cancer; immune response; HLA;
 CC Human leukocyte antigen.
 CC Homo sapiens.
 CC WO200283921-A2.
 DT 19-MAY-2003 (first entry)
 XX PD 24-OCT-2002.
 XX DR 10-APR-2002; 2002WO-US011654.
 XX AC 10-APR-2001; 2001US-0282739P.
 XX AC 10-APR-2001; 2001US-0283112P.
 XX AC 25-APR-2001; 2001US-0286630P.
 XX PA (AGEN-) AGENSY INC.
 XX DR 2003-075555/07.
 XX PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 XX PI Morrison K, Morrison RK, Raitano AB;
 XX PF 10-APR-2002; 2002WO-US011654.
 XX PR 10-APR-2001; 2001US-0282739P.
 XX PR 10-APR-2001; 2001US-0283112P.
 XX PR 25-APR-2001; 2001US-0286630P.
 XX PA (AGEN-) AGENSY INC.
 XX PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 XX PI Morrison K, Morrison RK, Raitano AB;
 XX DR 2003-075555/07.
 XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX Claim 13; Page 193; 1021PP; English.
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ7120-ABZ78168 and ABR01861). The genes and
 CC proteins are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or

XX XX Homo sapiens.
 AC XX WO200283921-A2.
 XX XX 24-OCT-2002.
 DT XX PD 24-OCT-2002.
 XX XX Human cancer-related protein 151P1C7A HLA peptide #1009.
 DB XX PR 10-APR-2002; 2002WO-US011654.
 XX XX PR 10-APR-2001; 2001US-0282739P.
 KW XX PR 10-APR-2001; 2001US-0283112P.
 human leukocyte antigen.
 XX XX PR 25-APR-2001; 2001US-0286630P.
 OS XX PA (AGEN-) AGENSYS INC.
 PN XX PA 24-OCT-2002.
 XX XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PD PI Morrison K, Morrison RK, Raitano AB;
 XX XX WPI; 2003-075555/07.
 PP XX New composition comprising a substance that modulates the structure of
 PR PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PR PT diagnostic reagents for eliciting cellular or humoral immune response in
 PR PA cancer patients.
 XX XX Claim 13; Page 197; 1021pp; English.
 PS XX The present invention relates to novel human cancer-related genes and
 PI XX CC proteins (ABZ78120-ABZ78168 and ABR01861). The genes and
 PI XX CC proteins are useful for eliciting a humoral or cellular immune response.
 DR XX The genes are useful as probes and primers for the amplification and/or
 XX XX detection of genes, mRNAs or their fragments, as reagents for the
 PT CC diagnosis of genes, mRNAs or their fragments, as coding sequences capable of
 PT CC directing the expression of the protein, as tools for modulating or
 PT CC inhibiting the expression of genes and/or translation of transcripts, and
 PA XX CC as therapeutic agents. The proteins and peptides are useful as
 XX XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 sequence is a human leukocyte antigen (HLA) peptide, used in an example
 from the invention.
 XX XX Sequence 9 AA;
 DR XX SQ Sequence 9 AA;
 XX XX Query Match 100.0%; Score 30; DB 6; Length 9;
 XX XX Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Mismatches 0; Gaps 0;
 XX XX AC ABR08558;
 XX XX AC 19-MAY-2003 (First entry)
 XX XX DB Human cancer-related protein 151P1C7A HLA peptide #1093.
 XX XX OS Homo sapiens.
 XX XX WO200283921-A2.
 AC XX 24-OCT-2002.
 XX XX PR 10-APR-2002; 2002WO-US011654.
 DT XX PR 10-APR-2001; 2001US-0282739P.
 XX XX PR 25-APR-2001; 2001US-0283112P.
 KW XX PR 10-APR-2001; 2001US-0286630P.
 human leukocyte antigen.
 XX XX

RESULT 13
 ABR08536
 ID ABR08536 standard; peptide; 9 AA.
 XX AC
 XX AC ABR08536;
 XX DT 19-MAY-2003 (first entry)
 XX DB Human cancer-related protein 151P1C7A HLA Peptide #1071.
 XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 human leukocyte antigen.
 XX KW

RESULT 14
 ABR08558
 ID ABR08558 standard; peptide; 9 AA.
 XX AC
 XX AC ABR08558;
 XX DT 19-MAY-2003 (First entry)
 XX DB Human cancer-related protein 151P1C7A HLA peptide #1093.
 XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 human leukocyte antigen.
 XX KW

RESULT 15
 ABR08536
 ID ABR08536 standard; peptide; 9 AA.
 XX AC
 XX AC ABR08536;
 XX DT 19-MAY-2003 (first entry)
 XX DB Human cancer-related protein 151P1C7A HLA Peptide #1071.
 XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 human leukocyte antigen.
 XX KW

CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 30; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRKR 6
 Db 4 RKRKR 9

RESULT 17

ABR08154

ABR08154 standard; peptide; 9 AA.

XX AC ABR08154;

XX DT 19-MAY-2003 (first entry)

XX Human cancer-related protein 151P1C7A HLA peptide #689.

DB XX Human; Cytostatic; vaccine; cancer; immune response; HLA;

KW XX human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PP 10-APR-2002; 2002WO-US011654.

XX PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX PA (AGEN-) AGENSY INC.

XX PI Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX DR 2003-075555/07.

XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.

XX PS Claim 13; Page 193; 1021PP; English.

XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the amplification and/or
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of gene and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 30; DB 8; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRKR 6
 Db 3 RKRKR 8

RESULT 19

ABR08921

ABR08921 standard; peptide; 10 AA.

XX AC ABR08921;

CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 30; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRKR 6
 Db 1 RKRKR 6

RESULT 18

ADK08966

ADK08966 standard; peptide; 9 AA.

XX AC ADK08966;

XX DT 06-MAY-2004 (first entry)

XX DE Human papillomavirus peptide #1021.

XX KW pathogenic virus; alternative reading frame; antigenic determinant;

KW virucide; vaccine; therapeutic agent; infection; HPV.

XX OS Human papillomavirus.

XX PN WO2004011650-A2.

XX PD 05-FEB-2004.

XX PF 24-JUL-2003; 2003WO-EP008112.

XX PR 24-JUL-2002; 2002AT-00001124.

PR 11-JUL-2003; 2003EP-00450171.

XX PA (INTB-) INTERCELL AG.

XX PI Mattner F, Schmidt W, Habel A;

XX DR WPI; 2004-169243/16.

XX New polypeptide encoded by an alternative reading frame of a pathogenic

PT virus comprising an antigenic determinant, useful for treating or

PT preventing an infection with the pathogenic virus.

XX PS Claim 18; Page 184; 220pp; English.

XX This invention relates to a novel polypeptide encoded by an alternative

CC reading frame of a pathogenic virus, where the polypeptide starts with a

CC methionine amino acid residue, which comprises an antigenic determinant

CC and more than 7 amino acid residues. The invention may be useful for the

CC production of compounds with a viricide activity or the development of a

CC vaccine. The polypeptide or its fragments may be useful as a therapeutic

CC agent. It is also useful for the manufacture of a medicament for treating

CC or preventing an infection with the pathogenic virus. The present

CC sequence is that of a human papillomavirus (HPV) epitope peptide of the

CC invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 30; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRKR 6
 Db 3 RKRKR 8

RESULT 19

ABR08921

ABR08921 standard; peptide; 10 AA.

XX AC ABR08921;

XX	19-MAY-2003	(first entry)	PN	WO200283921-A2.
DT			XX	XX
DB	Human cancer-related protein 151PIC7A HLA peptide #1456.		PD	24-OCT-2002.
XX			XX	
KW	Human; cytostatic; vaccine; cancer; immune response; HLA;		PF	10-APR-2002; 2002WO-US011654.
KW	human leukocyte antigen.		XX	
XX			PR	10-APR-2001; 2001US-0282739P.
OS	Homo sapiens.		PR	10-APR-2001; 2001US-0283112P.
XX			PR	25-APR-2001; 2001US-0286630P.
PN	WO200283921-A2.		XX	
XX	24-OCT-2002.		PA	(AGEN-) AGENSYS INC.
PD			XX	
XX	10-APR-2002; 2002WO-US011654.		PI	Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;
PF			PI	Morrison K, Morrison RK, Raitano AB;
XX			XX	
WPI	2003-075555/07.		XX	DR WPI; 2003-075555/07.
XX			XX	
PR	10-APR-2001; 2001US-0282739P.		PT	New composition comprising a substance that modulates the structure of
PR	10-APR-2001; 2001US-0283112P.		PT	proteins and polynucleotides, useful for therapeutic, prognostic and
PR	25-APR-2001; 2001US-0286630P.		PT	diagnostic reagents for eliciting cellular or humoral immune response in
XX			PT	cancer patients.
PA	(AGEN-) AGENSYS INC.		XX	
XX			PS	Claim 13; Page 196; 1021pp; English.
PI	Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;		XX	
PI	PI Morrison K, Morrison RK, Raitano AB;		XX	
XX			CC	The present invention relates to novel human cancer-related genes and
DR	WPI; 2003-075555/07.		CC	proteins (ABZ78120-ABZ78168 and ABR01861). The genes and
XX			CC	proteins are useful for eliciting a humoral or cellular immune response.
XX			CC	The genes are useful as probes and primers for the amplification and/or
PT	New composition comprising a substance that modulates the structure of		CC	detection of genes, mRNAs or their fragments, as reagents for the
PT	proteins and polynucleotides, useful for therapeutic, prognostic and		CC	diagnosis and/or prognosis of cancer, as coding sequences capable of
PT	PT diagnostic reagents for eliciting cellular or humoral immune response in		CC	directing the expression of the protein, as tools for modulating or
PT	cancer patients.		CC	inhibiting the expression of genes and/or translation of transcripts, and
PS	PS 201; 1021pp; English.		CC	as therapeutic agents. The proteins and peptides are useful as
XX	The present invention relates to novel human cancer-related genes and		CC	therapeutic, prognostic and diagnostic reagents for cancer. The present
CC	proteins (ABZ78120-ABZ78168 and ABR01861). The genes and		CC	sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC	proteins are useful for eliciting a humoral or cellular immune response.		CC	from the invention
CC	The genes are useful as probes and primers for the amplification and/or		XX	Sequence 10 AA;
CC	detection of genes, mRNAs or their fragments, as reagents for the		Query Match	100.0%; Score 30; DB 6; Length 10;
CC	diagnosis and/or prognosis of cancer, as coding sequences capable of		Best Local Similarity	100.0%; Pred. No. 86;
CC	directing the expression of the protein, as tools for modulating or		Matches	0; Mismatches 0; Indels 0; Gaps 0;
CC	inhibiting the expression of genes and/or translation of transcripts, and		QY	1 RKRKR 6
CC	as therapeutic agents. The proteins and peptides are useful as		Db	3 RKRKR 8
CC	therapeutic, prognostic and diagnostic reagents for cancer. The present			
CC	sequence is a human leukocyte antigen (HLA) peptide, used in an example			
CC	from the invention			
XX	Sequence 10 AA;			
QY	1 RKRKR 6			RESULT 21
Db	4 RKRKR 9			ABR0569
XX				ID ABR0569 standard; peptide: 10 AA.
AC	ABR08402			XX
XX	19-MAY-2003 (first entry)		AC	ABR0569;
XX			XX	DE Human cancer-related protein 151PIC7A HLA peptide #1104.
DE	Human cancer-related protein 151PIC7A HLA peptide #937.		XX	XX Human; cytostatic; vaccine; cancer; immune response; HLA;
XX			XX	KW human leukocyte antigen.
KW	Human; cytostatic; vaccine; cancer; immune response; HLA;		XX	XX 10-APR-2001; 2001US-0282739P.
KW	human leukocyte antigen.		XX	10-APR-2001; 2001US-0283112P.
XX			PR	25-APR-2001; 2001US-0286630P.
OS	Homo sapiens.		XX	XX
XX			PN	WO200283921-A2.
XX			XX	
DT	24-OCT-2002.		PD	24-OCT-2002.
XX			XX	
DE	Human cancer-related protein 151PIC7A HLA peptide #937.		XX	
XX			PP	10-APR-2002; 2002WO-US011654.
KW	Human; cytostatic; vaccine; cancer; immune response; HLA;		XX	XX 10-APR-2001; 2001US-0282739P.
KW	human leukocyte antigen.		XX	10-APR-2001; 2001US-0283112P.
XX			PR	25-APR-2001; 2001US-0286630P.
XX			XX	XX

PA (AGEN-) AGENSYS INC.
 XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 PT WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and/or diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.

Claim 13; Page 198; 1021PP; English.

The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention

SQ Sequence 10 AA;

Query Match 23
 Best Local Similarity 100.0%; Score 30; DB 6; Length 10;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRKR 6
 Db 3 RKRKR 8
 XX

RESULT 22
 ABR08053
 ID ABR08053 standard; peptide; 10 AA.
 XX
 AC ABR08053;
 XX
 DT 19-MAY-2003 (First entry)
 XX

DB Human cancer-related protein 151P1C7A HLA peptide #588.
 XX
 KW Human; Cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 XX
 PR 10-APR-2001; 2001US-0283112P.
 XX
 PR 25-APR-2001; 2001US-0286630P.
 XX
 (AGEN-) AGENSYS INC.

XX
 PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 PP 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 (AGEN-) AGENSYS INC.

XX
 PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 DR WPI; 2003-075555/07.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 (AGEN-) AGENSYS INC.

XX
 New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and/or diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.

PT XX cancer patients.

XX Claim 13; Page 192; 1021PP; English.

CC The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention

XX

SQ Sequence 10 AA;

Query Match 23
 Best Local Similarity 100.0%; Score 30; DB 6; Length 10;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRKR 6
 Db 2 RKRKR 7
 XX

RESULT 23
 ABR08455
 ID ABR08455 standard; peptide; 10 AA.
 XX
 AC ABR08455;
 XX
 DT 19-MAY-2003 (First entry)
 XX
 DE Human cancer-related protein 151P1C7A HLA peptide #990.

XX
 KW Human; Cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 Homo sapiens.
 XX
 WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PR 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 XX
 PR 10-APR-2001; 2001US-0283112P.
 XX
 PR 25-APR-2001; 2001US-0286630P.
 XX
 (AGEN-) AGENSYS INC.

XX
 PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 PP 2003-075555/07.

XX
 New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and/or diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.

XX
 PR 10-APR-2001; 2001US-0282739P.

XX
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 (AGEN-) AGENSYS INC.

XX
 PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

DR WPI; 2003-075555/07.
 XX
 New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and/or diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.

XX
 PR 10-APR-2001; 2001US-0282739P.

XX
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 (AGEN-) AGENSYS INC.

CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention

XX Sequence 10 AA;

Query Match 100.0%; Score 30; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 0;
 Gaps 0;

Qy 1 RKRKR 6

Db 4 RKRKR 9

RESIDUE 24
 ABR08599
 ID ABR08599 Standard; peptide; 10 AA.
 XX
 AC ABR08599;
 XX
 DT 19-MAY-2003 (First entry)
 XX
 DE Human cancer-related protein 151PICTA HLA peptide #1134.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PR 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYS INC.

PA

XX

W0200283921-A2.

XX

PD 24-OCT-2002.

XX

PP 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 25-APR-2001; 2001US-0286630P.

XX

(AGEN-) AGENSYS INC.

PA

XX

PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;

XX

PI Morrison K, Morrison RK, Raitano AB;

XX

DR 2003-075555/07.

XX

WPI; 2003-075555/07.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

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PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;

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PI Morrison K, Morrison RK, Raitano AB;

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DR 2003-075555/07.

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WPI; 2003-075555/07.

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PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

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PS 198; 1021pp; English.

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PI Morrison K, Morrison RK, Raitano AB;

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DR 2003-075555/07.

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WPI; 2003-075555/07.

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PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

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PS 198; 1021pp; English.

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PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;

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PI Morrison K, Morrison RK, Raitano AB;

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XX

WPI; 2003-075555/07.

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PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PS 198; 1021pp; English.

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PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;

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PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;

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PI Morrison K, Morrison RK, Raitano AB;

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PI Morrison K, Morrison RK, Raitano AB;

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PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

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PI Morrison K, Morrison RK, Raitano AB;

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PR 25-APR-2001; 2001US-0286630P.

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PI Morrison K, Morrison RK, Raitano AB;

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DR 2003-075555/07.

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WPI; 2003-075555/07.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
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SQ Sequence 10 AA;
Query Match 100.0%; Score 30; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RIGRK 6
| | | | |
Db 4 RIGRK 9

Search completed: April 13, 2006, 08:45:09
Job time : 190 secs

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2	30	100.0	9	1 US-08-332-518-10	Sequence 10, Appli	
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4	30	100.0	21	1 US-08-945-168-72	Sequence 66, Appli	
5	30	100.0	21	1 US-08-678-974D-66	Sequence 72, Appli	
6	27	90.0	8	2 US-10-028-056-25	Sequence 25, Appli	
7	27	90.0	9	1 US-08-332-518-8	Sequence 2, Appli	
8	27	90.0	9	1 US-08-332-518-9	Sequence 8, Appli	
9	27	90.0	9	1 US-08-332-518-11	Sequence 9, Appli	
10	27	90.0	9	1 US-08-332-709-31	Sequence 11, Appli	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

FILING DATE: 23-APR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,7658
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 677-5300
 TELEX: (202) 672-5399
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-332-518-10

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 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRKR 6
 Db 2 RKRKR 7

RESULT 3
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 / Sequence 11, Application US/083378709
 / Patent No. 5831001
 / GENERAL INFORMATION:
 / APPLICANT: TWIST, Michael
 / APPLICANT: BARNETT, Richard
 / APPLICANT: REID, Lorrie
 / APPLICANT: SUMNER-SMITH, Martin
 / TITLE OF INVENTION: TREATMENT OF HERPES VIRUS INFECTION
 / NUMBER OF SEQUENCES: 33
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Foley & Lardner
 / STREET: 1800 Diagonal Road, Suite 500
 / CITY: Alexandria
 / STATE: VA
 / COUNTRY: USA
 / ZIP: 22313-0299

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/378,709
 FILING DATE: 24-OCT-1990
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/872,398
 FILING DATE: 23-APR-1992
 APPLICATION NUMBER: US 07/779,735
 FILING DATE: 23-OCT-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/602,953
 FILING DATE: 24-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,7658
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-9300
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid

TOPOLOGY: linear
 US-08-378-709-11
 / Sequence 66, Application US/07678974D
 / Patent No. 5629116
 / GENERAL INFORMATION:
 / APPLICANT: DILLNER, JOAKIM
 / APPLICANT: DILLNER, LENA
 / TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN PAPILLOMAVIRUS
 / NUMBER OF SEQUENCES: 67
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: HERMAN & AISENBERG
 / STREET: 1730 RHODE ISLAND AVENUE, N.W.,
 / CITY: WASHINGTON
 / STATE: D.C.
 / COUNTRY: U.S.A.
 / ZIP: 20036-3186
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 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/678,974D
 FILING DATE: 25-JUN-1991
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: AISENBERG, Irwin M.
 / REGISTRATION NUMBER: 19,007
 / REFERENCE/DOCKET NUMBER: SG19171
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 202-293-1404
 / TELEFAX: 202-872-0493
 / TELEX: 440 069 AIS UI
 / INFORMATION FOR SEQ ID NO: 66:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 21 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 US-07-678-974D-66

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Qy 1 RKRKR 6
 Db 4 RKRKR 9

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 / Sequence 72, Application US/08945168
 / Patent No. 5898548
 / GENERAL INFORMATION:
 / APPLICANT: DILLNER, JOAKIM
 / TITLE OF INVENTION: PEPTIDE-BASED VACCINE AGAINST PAPILLOMA
 / NUMBER OF SEQUENCES: 117
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P. C.
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
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 APPLICATION NUMBER: US/08/945,168
 FILING DATE: 18-DEC-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/00533
 FILING DATE: 23-APR-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: SE 9501512-9
 FILING DATE: 24-APR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 7752-0002-0 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 INFORMATION FOR SEQ ID NO: 72:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-945-168-72

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Db 4 RKRKR 9

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 / General INFORMATION:
 / APPLICANT: REUB, KAREN
 / APPLICANT: PTERY, MIKLOS
 / TITLE OF INVENTION: A NOVEL GENE ASSOCIATED WITH REGULATION OF ADIPOSITY AND INSULIN
 / FILE REFERENCE: 407T-898010US
 / CURRENT APPLICATION NUMBER: US/10/028,056
 / CURRENT FILING DATE: 2001-12-19
 / PRIOR APPLICATION NUMBER: US 60/257,772
 / PRIOR FILING DATE: 2000-12-22
 / NUMBER OF SEQ ID NOS: 25
 / SOFTWARE: Patentin version 3.0
 / SEQ ID NO: 25
 / LENGTH: 8
 / TYPE: PRT
 / ORGANISM: Homo sapiens

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 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 US-10-028-056-25

Qy 1 RKRKR 6
 Db 2 RKRKR 7

RESULT 8
 US-08-332-518-8

Db 1 RKRKR 6

RESULT 7
 US-08-332-518-2
 / Sequence 2, Application US/08332518
 / Patent No. 5633210
 / GENERAL INFORMATION:
 / APPLICANT: TWIST, Michael
 / APPLICANT: SUMNER, SMITH, Martin
 / TITLE OF INVENTION: TREATMENT OF CYTOMEGALOVIRUS INFECTION
 / NUMBER OF SEQUENCES: 26
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Foley Lardner
 / STREET: 3000 K Street, N.W., Suite 500
 / CITY: Washington
 / STATE: D.C.
 / COUNTRY: USA
 / ZIP: 20007-5109
 / COMPUTER READABLE FORM:
 / COMPUTER TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/332,518
 / FILING DATE: 31-OCT-1994
 / CLASSIFICATION: 514
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 08/139,757
 / FILING DATE: 22-OCT-1993
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US/08/332,518
 / FILING DATE: 31-OCT-1994
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 07/872,398
 / FILING DATE: 23-APR-1992
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 07/779,735
 / FILING DATE: 23-OCT-1991
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 07/602,953
 / FILING DATE: 24-OCT-1990
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 07/995,742
 / FILING DATE: 22-DEC-1992
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 07/872,318
 / FILING DATE: 23-APR-1992
 / ATTORNEY/AGENT INFORMATION:
 / NAME: BENT, Stephen A.
 / REGISTRATION NUMBER: 29,768
 / REFERENCE/DOCKET NUMBER: 16777/266/ALLE
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (202) 672-5300
 / TELEFAX: (202) 672-5399
 / TELEX: 904136
 / INFORMATION FOR SEQ ID NO: 2:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 9 amino acids
 / TYPE: amino acid
 / STRANDEDNESS:
 / TOPOLOGY: linear
 US-08-332-518-2

Query Match Score 27; DB 1; Length 9;
 Best Local Similarity 83.3%; Pred. No. 4.6e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

/*
Sequence 8, Application US/08332518
  / Paten No. 5633230
  / GENERAL INFORMATION:
  / APPLICANT: TWIST, Michael
  / APPLICANT: SUMNER-SMITH, Martin
  / TITLE OF INVENTION: TREATMENT OF CYTOMEGALOVIRUS INFECTION
  / NUMBER OF SEQUENCES: 26
  / CORRESPONDENCE ADDRESS:
  / ADDRESSSE: Foley & Lardner
  / STREET: 3000 K Street, N.W., Suite 500
  / CITY: Washington
  / STATE: D.C.
  / COUNTRY: USA
  / ZIP: 20007-5109
  / COMPUTER READABLE FORM:
  / MEDIUM TYPE: Floppy disk
  / COMPUTER: IBM PC compatible
  / OPERATING SYSTEM: PC-DOS/MS-DOS
  / SOFTWARE: PatentIn Release #1., Version #1.30
  / CURRENT APPLICATION DATA:
  / APPLICATION NUMBER: US/08/332,518
  / FILING DATE: 31-OCT-1994
  / PRIOR APPLICATION DATA:
  / APPLICATION NUMBER: US 08/139,757
  / FILING DATE: 22-OCT-1993
  / PRIOR APPLICATION DATA:
  / APPLICATION NUMBER: US 07/872,398
  / FILING DATE: 23-APR-1992
  / PRIOR APPLICATION DATA:
  / APPLICATION NUMBER: US 07/779,735
  / FILING DATE: 23-OCT-1991
  / PRIOR APPLICATION DATA:
  / APPLICATION NUMBER: US 07/602,953
  / FILING DATE: 24-OCT-1990
  / PRIOR APPLICATION DATA:
  / APPLICATION NUMBER: US 07/995,742
  / FILING DATE: 22-DEC-1992
  / PRIOR APPLICATION DATA:
  / APPLICATION NUMBER: US 07/872,318
  / FILING DATE: 23-APR-1992
  / ATTORNEY/AGENT INFORMATION:
  / NAME: BENT, Stephen A.
  / REGISTRATION NUMBER: 29,796
  / REFERENCE/DOCKET NUMBER: 16,777/266/ALL
  / TELECOMMUNICATION INFORMATION:
  / TELEPHONE: (202) 672-5300
  / TELEFAX: (202) 672-5399
  / TELEX: 904136
  / INFORMATION FOR SEQ ID NO: 8:
  / SEQUENCE CHARACTERISTICS:
  / LENGTH: 9 amino acids
  / TYPE: amino acid
  / STRANDEDNESS:
  / TOPOLOGY: linear
US-08-332-518-8

Query Match 90.0% ; Score 27; DB 1; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0

Qy 1 RRRRR 6
Db 1 RRRRR 6

RESULT 9
US-08-332-518-9
Sequence 9, Application US/08332518
  / Paten No. 5633230
  / GENERAL INFORMATION:
  / APPLICANT: TWIST, Michael
  / APPLICANT: SUMNER-SMITH, Martin

```

TITLE OF INVENTION: TREATMENT OF CYTOMEGALOVIRUS INFECTION
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.10
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/332,518
 FILING DATE: 31-OCT-1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/139,757
 FILING DATE: 22-OCT-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/872,398
 FILING DATE: 23-APR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/779,735
 FILING DATE: 23-OCT-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/602,953
 FILING DATE: 24-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/995,742
 FILING DATE: 22-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/872,318
 FILING DATE: 23-APR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 16777/266/ALLE
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5300
 TELEFAX: (202) 672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDBEADNESS:
 TOPOLOGY: linear
 US-08-332-518-9

Query	Match	Score	Length
Qy	Best Local Similarity	90.0%	27
Qy	Matches	83.3%	DB 1;
Qy	Conservative	1;	Length 9;
Db	Mismatches	4.6e+05;	Pat. No. 4
Db	Indels	0;	Length 0;

RESULT 10
 US-08-332-518-11
 / sequence 11, Application US/08332518
 / Patent No. 5633230
 / GENERAL INFORMATION:
 / APPLICANT: TWIST, Michael
 / APPLICANT: SUMNER-SMITH, Martin
 / TITLE OF INVENTION: TREATMENT OF CYTOMEGALOVIRUS INFECTION
 / NUMBER OF SEQUENCES: 26
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEES: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500

CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/332,518
 FILING DATE: 31-OCT-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/139,757
 FILING DATE: 22-OCT-1993

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/872,398
 FILING DATE: 23-APR-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/779,735
 FILING DATE: 23-OCT-1991

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/995,742
 FILING DATE: 22-DEC-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/602,953
 FILING DATE: 24-OCT-1990

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/799,742
 FILING DATE: 22-DEC-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/872,318
 FILING DATE: 23-APR-1992

ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,7658
 REFERENCE/DOCKET NUMBER: 16777/266/ALLE
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5300
 TELEX: 904156
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear

US-08-332-518-11

Query Match 90.0%; Score 27; DB 1; Length 9;
 Best Local Similarity 83.3%; Pred. No. 4.6e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRKR 6
 Db 2 RRRRKR 7

RESULT 11
 US-08-378-709-3
 Sequence 3, Application US/08378709
 / GENERAL INFORMATION:
 / Patent No. 5831001
 / APPLICANT: TWIST, Michael
 / APPLICANT: BARNETT, Richard
 / APPLICANT: REID, Lorne
 / APPLICANT: SUMNER-SMITH, Martin
 / TITLE OF INVENTION: TREATMENT OF HERPES VIRUS INFECTION
 / NUMBER OF SEQUENCES: 33
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Foley & Lardner
 / STREET: 1800 Diagonal Road, Suite 500
 / CITY: Alexandria
 / STATE: VA USA
 / ZIP: 22313-0299

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/378,709

CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/872,398
 FILING DATE: 23-APR-1992

APPLICATION NUMBER: US 07/779,735
 FILING DATE: 24-OCT-1990

ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,7658
 REFERENCE/DOCKET NUMBER: 16777/176/ALLE
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-9300
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

US-08-378-709-3

Query Match 90.0%; Score 27; DB 1; Length 9;
 Best Local Similarity 83.3%; Pred. No. 4.6e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRKR 6
 Db 2 RRRRKR 7

RESULT 12
 US-08-378-709-9
 Sequence 9, Application US/08378709
 / GENERAL INFORMATION:
 / Patent No. 5831001
 / APPLICANT: TWIST, Michael
 / APPLICANT: BARNETT, Richard
 / APPLICANT: REID, Lorne
 / APPLICANT: SUMNER-SMITH, Martin
 / TITLE OF INVENTION: TREATMENT OF HERPES VIRUS INFECTION
 / NUMBER OF SEQUENCES: 33
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Foley & Lardner
 / STREET: 1800 Diagonal Road, Suite 500
 / CITY: Alexandria
 / STATE: VA USA
 / ZIP: 22313-0299

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/378,709

CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/872,398
 FILING DATE: 23-APR-1992

APPLICATION NUMBER: US 07/779,735

FILING DATE: 23-OCT-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/602, 953
 FILING DATE: 24-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29, 768
 REFERENCE/DOCKET NUMBER: 16777/176 ALLE
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-9300
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-378-709-9

Query Match 90.0%; Score 27; DB 1; Length 9;
 Best Local Similarity 83.3%; Pred. No. 4.6e+05;
 Matches 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRRKR 6
 Db 2 RKRRRK 7

RESULT 14
 US-08-378-709-12

Sequence 12, Application US/08378709
 Patent No. 5831001

GENERAL INFORMATION:
 APPLICANT: TWIST, Michael
 ATTORNEY: REID, Lorne
 APPLICANT: SUMNER-SMITH, Martin
 TITLE OF INVENTION: TREATMENT OF HERPES VIRUS INFECTION
 NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 1800 Diagonal Road, Suite 500
 CITY: Alexandria
 STATE: VA
 ZIP: 22313-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/378,709
 FILING DATE: 23-OCT-1991
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/872,398
 FILING DATE: 23-APR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29, 768
 REFERENCE/DOCKET NUMBER: 16777/176 ALLE
 TELEPHONE: (703) 836-9300
 TELEFAX: 899149
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-378-709-12

Query Match 90.0%; Score 27; DB 1; Length 9;
 Best Local Similarity 83.3%; Pred. No. 4.6e+05;
 Matches 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRRKR 6
 Db 2 RKRRRK 7

RESULT 13
 US-08-378-709-10

Sequence 10, Application US/08378709
 Patent No. 5831001

GENERAL INFORMATION:
 APPLICANT: TWIST, Michael
 ATTORNEY: REID, Lorne
 APPLICANT: SUMNER-SMITH, Martin
 TITLE OF INVENTION: TREATMENT OF HERPES VIRUS INFECTION
 NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 1800 Diagonal Road, Suite 500
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22313-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/378,709
 FILING DATE: 23-OCT-1991
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/602,953
 FILING DATE: 24-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29, 768
 REFERENCE/DOCKET NUMBER: 16777/176 ALLE
 TELEPHONE: (703) 836-9300
 TELEFAX: 899149
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-378-709-10

Query Match 90.0%; Score 27; DB 1; Length 9;
 Best Local Similarity 83.3%; Pred. No. 4.6e+05;
 Matches 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRRKR 6
 Db 2 RKRRRK 7

RESULT 12
 US-08-378-709-9

Sequence 9, Application US/08378709
 Patent No. 5831001

GENERAL INFORMATION:
 APPLICANT: TWIST, Michael
 ATTORNEY: REID, Lorne
 APPLICANT: SUMNER-SMITH, Martin
 TITLE OF INVENTION: TREATMENT OF HERPES VIRUS INFECTION
 NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 1800 Diagonal Road, Suite 500
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22313-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 07/602,953
 FILING DATE: 24-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29, 768
 REFERENCE/DOCKET NUMBER: 16777/176 ALLE
 TELEPHONE: (703) 836-9300
 TELEFAX: 899149
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-378-709-9

Query Match 90.0%; Score 27; DB 1; Length 9;
 Best Local Similarity 83.3%; Pred. No. 4.6e+05;
 Matches 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRRKR 6
 Db 2 RKRRRK 7

RESULT 15
 PCT-US91-08328-15
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruggeri, Zaverio M.
 ; APPLICANT: Houghten, Richard A.
 ; TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING
 ; TITLE OF INVENTION: OF ADHESION MOLECULES
 ; NUMBER OF SEQUENCES: 47
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN
 ; STREET: 345 Park Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US91/08328
 ; FILING DATE: 19911107
 ; CLASSIFICATION: 514
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/610,363
 ; FILING DATE: 07-NOV-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Moroz, Eugene
 ; REGISTRATION NUMBER: 25,237
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212)758-4800
 ; TELEFAX: (212)751-6849
 ; INFORMATION FOR SEQ ID NO: 15:
 ; LENGTH: 11 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FEATURE: Cross-links
 ; NAME/KEY: Cross-links
 ; LOCATION: 5..>11
 ; OTHER INFORMATION: /note= "Sequence linked by
 ; interchain amide bond at Lys residue with Glu
 ; OTHER INFORMATION: residue on Arg4-Glu-Arg-Ser-Arg-Gly-Asp-Val
 ; PUBLICATION INFORMATION:
 ; DOCUMENT NUMBER: US 4,683,291
 ; FILING DATE: 28-OCT-1985
 ; PUBLICATION DATE: 28-JUL-1987
 ; PUBLICATION INFORMATION:
 ; DOCUMENT NUMBER: US B1 4,683,291
 ; FILING DATE: 28-OCT-1985
 ; PUBLICATION DATE: 03-JUL-1990
 ; PCT-US91-08328-21

Query Match Similarity 90.0%; Score 27; DB 4; Length 11;
 Best Local Similarity 83.3%; Pred. No. 89; Mismatches 1; Indels 0; Gaps 0;
 PCT-US91-08328-15

Qy 1 RKRKR 6
 Best Local Similarity 83.3%; Pred. No. 89; Mismatches 1; Indels 0; Gaps 0;
 Db 1 RKRKR 6

RESULT 17
 US-09-816-688b-1.rai
 ; Sequence 31, Application US/08378709
 ; GENERAL INFORMATION:
 ; APPLICANT: TWIST, Michael
 ; APPLICANT: BARNETT, Richard
 ; APPLICANT: REID, Lorne

RESULT 16
 PCT-US91-08328-21
 ; Sequence 21, Application PC/TUSS9108328
 ; GENERAL INFORMATION:

APPLICANT: SUMNER-SMITH, Martin
 TITLE OF INVENTION: TREATMENT OF HERPES VIRUS INFECTION
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 1800 Diagonal Road, Suite 500
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22213-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ParentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/378,709
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/872,398
 FILING DATE: 23-APR-1992
 APPLICATION NUMBER: US 07/779,735
 FILING DATE: 23-OCT-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/602,953
 FILING DATE: 24-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 16777/176 ALTB
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-9300
 TELEFAX: (703) 683-4109
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-378-709-31

Query Match 90.0%; Score 27; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 96;
 Matches 5; Conservative 1; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 RKRKR 6
 Db 4 KRRKR 9

RESULT 18
 US-09-325-601-50
 Sequence 50, Application US/09325601
 Patent No. 6573045
 GENERAL INFORMATION:
 APPLICANT: Prescott
 TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
 FILE REFERENCE: 3950/81235
 CURRENT APPLICATION NUMBER: US/09/325,601
 CURRENT FILING DATE: 1999-06-03
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.1
 LENGTH: 13

TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
 SEQ ID NO 50
 LENGTH: 13
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
 US-09-325-601-50

RESULT 21
 US-09-325-601-42
 Sequence 42, Application US/09325601
 Patent No. 6573045
 GENERAL INFORMATION:
 APPLICANT: Prescott
 TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
 FILE REFERENCE: 3950/81235
 CURRENT APPLICATION NUMBER: US/09/325,601
 CURRENT FILING DATE: 1999-06-03
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 42
 LENGTH: 13
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
 OTHER INFORMATION: Q, R-pentapeptide library
 US-09-325-601-42

RESULT 21
 US-09-325-601-46
 Sequence 46, Application US/09325601
 Patent No. 6573045
 GENERAL INFORMATION:
 APPLICANT: Prescott
 TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
 FILE REFERENCE: 3950/81235
 CURRENT APPLICATION NUMBER: US/09/325,601
 CURRENT FILING DATE: 1999-06-03
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.1
 LENGTH: 13
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
 OTHER INFORMATION: Q, R-pentapeptide library
 US-09-325-601-46

RESULT 19
 US-09-325-601-37
 Sequence 37, Application US/09325601
 Patent No. 6573045
 GENERAL INFORMATION:
 APPLICANT: Karn
 APPLICANT: Prescott
 TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
 FILE REFERENCE: 3950/81235
 CURRENT APPLICATION NUMBER: US/09/325,601
 CURRENT FILING DATE: 1999-06-03
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 37
 LENGTH: 13
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
 OTHER INFORMATION: Q, R-pentapeptide library
 US-09-325-601-37

Query Match 90.0%; Score 27; DB 2; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 RKRKR 6
 Db 2 RKRKR 7

RESULT 20
 US-09-325-601-42
 Sequence 42, Application US/09325601
 Patent No. 6573045
 GENERAL INFORMATION:
 APPLICANT: Karn
 APPLICANT: Prescott
 TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
 FILE REFERENCE: 3950/81235
 CURRENT APPLICATION NUMBER: US/09/325,601
 CURRENT FILING DATE: 1999-06-03
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 42
 LENGTH: 13
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
 OTHER INFORMATION: Q, R-pentapeptide library
 US-09-325-601-42

Query Match 86.7%; Score 26; DB 2; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 RKRKR 6
 Db 2 RKRKR 7

RESULT 20
 US-09-325-601-42
 Sequence 42, Application US/09325601
 Patent No. 6573045
 GENERAL INFORMATION:
 APPLICANT: Karn
 APPLICANT: Prescott
 TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
 FILE REFERENCE: 3950/81235
 CURRENT APPLICATION NUMBER: US/09/325,601
 CURRENT FILING DATE: 1999-06-03
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 42
 LENGTH: 13
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
 OTHER INFORMATION: Q, R-pentapeptide library
 US-09-325-601-42

Query Match 86.7%; Score 26; DB 2; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 RKRKR 6
 Db 2 RKRKR 7

Sequence 46, Application US/09325601
 ; Patent No. 6573045
 ; GENERAL INFORMATION:
 ; APPLICANT: Prescott
 ; TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
 ; FILE REFERENCE: 3950/81235
 ; CURRENT APPLICATION NUMBER: US/09/325,601
 ; CURRENT FILING DATE: 1999-06-03
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 46
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
 ; OTHER INFORMATION: Q, R-pentapeptide library
 US-09-325-601-46

Query Match 86.7%; Score 26; DB 2; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RKRKKR 6
 Db 2 RKRKRQ 7

RESULT 22
 US-09-325-601-48
 ; Sequence 48, Application US/09325601
 ; Patent No. 6573045
 ; GENERAL INFORMATION:
 ; APPLICANT: Prescott
 ; TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
 ; FILE REFERENCE: 3950/81235
 ; CURRENT APPLICATION NUMBER: US/09/325,601
 ; CURRENT FILING DATE: 1999-06-03
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 48
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
 ; OTHER INFORMATION: Q, R-pentapeptide library
 US-09-325-601-48

Query Match 86.7%; Score 26; DB 2; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RKRKKR 6
 Db 2 RKRKRQ 7

RESULT 23
 US-09-595-043A-30
 ; Sequence 30, Application US/08595043A
 ; Patent No. 5335824
 ; GENERAL INFORMATION:
 ; APPLICANT: SGARLATO, GREGORY D.
 ; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
 ; NUMBER OF SEQUENCES: 90
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEES: MEDLEN & CARROLL
 ; STREET: 220 MONTGOMERY STREET, SUITE 2200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA

Query Match 83.3%; Score 25; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 KRRKR 6
 Db 1 KRRKR 5

RESULT 25
 US-09-351-414-8
 ; Sequence 8, Application US/09351414
 ; Patent No. 6265199
 ; GENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.
 APPLICANT: Deindur, Nand
 APPLICANT: Delsher, Theresa A.
 APPLICANT: Bishop, Paul D.
 TITLE OF INVENTION: DISINTEGRIN HOMOLOG
 FILE REFERENCE: 98-29
 CURRENT APPLICATION NUMBER: US/09/351,414
 CURRENT FILING DATE: 1999-07-09
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 8 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: antigenic peptide
 US-09-351-14-8

Query Match 83.3%; Score 25; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKRRKR 6
 Db 2 RKREKR 6

RESULT 26
 US-08-249-387-6
 Sequence 6, Application US/08249387
 Patent No. 5681700
 GENERAL INFORMATION:
 APPLICANT: Reichlin, Morris
 ATTORNEY: Koren, Eugen
 TITLE OF INVENTION: Assay for Pathogenicity of Anti-DNA
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Patrea L. Pabst
 STREET: 1100 Peachtree Street, Suite 2800
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA
 ZIP: 30309-4520

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0,
 Version #1.25
 CURRENT APPLICATION NUMBER: US/09/366,103
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/450,188
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Patrea L.
 REGISTRATION NUMBER: 31,284
 REFERENCE/DOCKET NUMBER: ORRF145
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 815-5508
 TELEFAX: (404) 815-6555
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDBEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 US-09-366-103-6

Query Match 83.3%; Score 25; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 4.6e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRRKR 6
 Db 2 RKREKR 7

RESULT 27
 US-09-366-103-6
 Sequence 6, Application US/09366103
 Patent No. 6280944
 GENERAL INFORMATION:
 APPLICANT: Reichlin, Morris
 ATTORNEY: Koren, Eugen
 TITLE OF INVENTION: Assay for Pathogenicity of Anti-DNA Antibodies
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Patrea L. Pabst
 STREET: 1100 Peachtree Street,
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA
 ZIP: 30309-4530

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0,
 Version #1.25
 CURRENT APPLICATION NUMBER: US/09/366,103
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/450,188
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Patrea L.
 REGISTRATION NUMBER: 31,284
 REFERENCE/DOCKET NUMBER: ORRF145
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 815-5508
 TELEFAX: (404) 815-6555
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDBEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 US-09-366-103-6

Query Match 83.3%; Score 25; DB 1; Length 8;
 Best Local Similarity 83.3%; Pred. No. 4.6e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRRKR 6
 Db 2 RKREKR 7

RESULT 28
 PCT-US91-08328-17
 Sequence 17, Application PC/TUS9108328
 GENERAL INFORMATION:
 APPLICANT: Ruggeri, Zaverio M.
 ATTORNEY: Houghten, Richard A.
 TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING
 US-08-249-387-6

Query Match 83.3%; Score 25; DB 1; Length 8;

/TITLE OF INVENTION: OF ADHESION MOLECULES
 /NUMBER OF SEQUENCES: 47
 /ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN
 /STREET: 345 Park Avenue
 /CITY: New York
 /COUNTRY: USA
 /ZIP: 10154
 /COMPUTER READABLE FORM:
 /MEDIUM TYPE: Floppy disk
 /OPERATING SYSTEM: IBM PC compatible
 /SOFTWARE: PC-DOS/MS-DOS
 /CURRENT APPLICATION DATA:
 /APPLICATION NUMBER: PCT/US91/08328
 /FILING DATE: 1991-11-07
 /CLASSIFICATION: 514
 /PRIOR APPLICATION DATA:
 /APPLICATION NUMBER: US 07/610,363
 /FILING DATE: 07-NOV-1990
 /ATTORNEY/AGENT INFORMATION:
 /NAME: Moroz, Eugene
 /REGISTRATION NUMBER: 25,237
 /REFERENCE/DOCKET NUMBER: 1198 4079PC
 /TELECOMMUNICATION INFORMATION:
 /TELEPHONE: (212)758-4800
 /TELEFAX: (212)751-6849
 /TELEX: 421792
 /SEQUENCE INFORMATION:
 /SEQUENCE FOR SEQ ID NO: 17:
 /SEQUENCE CHARACTERISTICS:
 /LENGTH: 11 amino acids
 /TYPE: AMINO ACID
 /TOPOLOGY: unknown
 /MOLECULE TYPE: peptide
 /HYPOTHETICAL: NO
 /ANTI-SENSE: NO
 /FEATURE:
 /NAME/KEY: Cross-links
 /LOCATION: 4..>11
 /OTHER INFORMATION: /note= "Sequence linked by interchain amide bond at Lys residue with Glu residue on Arg3-Glu-Arg2-Ser-Arg-Gly-Asp-Val"
 /PUBLICATION INFORMATION:
 /DOCUMENT NUMBER: US 4,683,291
 /FILING DATE: 28-OCT-1985
 /PUBLICATION DATE: 28-JUL-1987
 /DOCUMENT NUMBER: US B1 4,683,291
 /FILING DATE: 28-OCT-1985
 /PUBLICATION DATE: 03-JUL-1990
 /PCT-US91-08328-17

/NUMBER OF SEQ ID NOS: 53
 /SOFTWARE: PatentIn Ver. 2.1
 /SEQ ID NO: 19
 /LENGTH: 13
 /TYPE: PRT
 /ORGANISM: Artificial Sequence
 /FEATURE:
 /OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
 /OTHER INFORMATION: Q, R-pentapeptide library
 /US-09-325-601-19

Query Match 83.3%; Score 25; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRRK 5
 Db 6 RKRRK 10

RESULT 30
 US-09-325-601-28
 /Sequence 28, Application US/09325601
 /Patent No. 6573045
 /GENERAL INFORMATION:
 /APPLICANT: Karn
 /APPLICANT: Prescott
 /TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
 /FILE REFERENCE: 3950/81235
 /CURRENT APPLICATION NUMBER: US/09/325,601
 /CURRENT FILING DATE: 1999-06-03
 /NUMBER OF SEQ ID NOS: 53
 /SOFTWARE: PatentIn Ver. 2.1
 /SEQ ID NO: 28
 /LENGTH: 13
 /TYPE: PRT
 /ORGANISM: Artificial Sequence
 /FEATURE:
 /OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
 /OTHER INFORMATION: Q, R-pentapeptide library
 /US-09-325-601-28

Query Match 83.3%; Score 25; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRRK 5
 Db 6 RKRRK 10

Search completed: April 13, 2006, 08:50:34
 Job time : 47 secs

RESULT 29
 US-09-325-601-19
 /Sequence 19, Application US/09325601
 /Patent No. 6573045
 /GENERAL INFORMATION:
 /APPLICANT: Karn
 /APPLICANT: Prescott
 /TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
 /FILE REFERENCE: 3950/81235
 /CURRENT APPLICATION NUMBER: US/09/325,601
 /CURRENT FILING DATE: 1999-06-03

Query Match 83.3%; Score 25; DB 4; Length 11;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKRRK 6
 Db 3 RKRRSR 8

Result No.	Score	Query Match	Length	DB ID	Description
1	27	90.0	8	US-10-512-299A-45	Sequence 45, App1
2	26	86.7	10	US-10-918-638-1	Sequence 1, App1
3	26	86.7	10	US-10-246-300D-1	Sequence 1, App1
4	26	86.7	20	US-11-223-699A-66	Sequence 66, App1
5	26	86.7	20	US-11-121-566A-66	Sequence 66, App1
6	25	83.3	5	US-11-179-639-21	Sequence 21, App1
7	25	83.3	6	US-11-242-243-7	Sequence 7, App1
8	25	83.3	6	US-11-242-243-8	Sequence 8, App1
9	25	83.3	21	US-10-512-299A-55	Sequence 55, App1
10	24	80.0	6	US-10-850-207-8	Sequence 8, App1
11	24	80.0	7	US-11-943-112A-44	Sequence 44, App1
12	24	80.0	7	US-11-041-103-5	Sequence 5, App1
13	24	80.0	7	US-11-107-371-6	Sequence 6, App1
14	24	80.0	7	US-11-141-725-10	Sequence 10, App1
15	24	80.0	7	US-11-223-699A-12	Sequence 12, App1
16	24	80.0	7	US-11-223-699A-64	Sequence 64, App1
17	24	80.0	7	US-11-121-566A-12	Sequence 12, App1
18	24	80.0	7	US-11-121-566A-64	Sequence 64, App1
19	24	80.0	8	US-11-019-899A-26	Sequence 26, App1
20	24	80.0	8	US-11-155-845-2	Sequence 2, App1
21	24	80.0	8	US-11-075-649A-8	Sequence 8, App1
22	24	80.0	9	US-10-985-426-7	Sequence 7, App1
23	24	80.0	9	US-10-509-78A-140	Sequence 140, App1
24	24	80.0	9	US-10-512-299A-12	Sequence 12, App1
25	24	80.0	9	US-11-016-542-20	Sequence 20, App1

RESULT 1 US-0512-299A-45
 / Sequence 45, Application US/10512299A
 / Publication No. US20060057668A1
 / GENERAL INFORMATION:
 / APPLICANT: TOAGOSEI CO., LTD.
 / APPLICANT: YOSHIDA, Tetsuniko
 / APPLICANT: KUME, Masayoshi
 / APPLICANT: YAMADA, Hiroki
 / APPLICANT: KOURAI, Hiroki
 / TITLE OF INVENTION: ANTIMICROBIAL POLYPEPTIDE AND UTILIZATION THEREOF
 / FILE REFERENCE: 54003-8003 US00
 / CURRENT FILING DATE: 2004-10-21
 / PRIOR APPLICATION NUMBER: PCT/JP03/05225
 / PRIOR FILING DATE: 2003-04-24

RESULT 2 US-10-918-638-1
 / Sequence 1, Application US/10918638
 / Publication No. US20050249663A1
 / GENERAL INFORMATION:
 / APPLICANT: Copharos
 / TITLE OF INVENTION: COBALAMIN MEDIATED DELIVERY OF NUCLEAR ACIDS, ANALOGS
 / TITLE OF INVENTION: AND
 / TITLE OF INVENTION: DERIVATIVES THEREOF
 / FILE REFERENCE: COP1010
 / CURRENT APPLICATION NUMBER: US/10/918,638
 / CURRENT FILING DATE: 2004-08-12
 / PRIOR APPLICATION NUMBER: US/10/246,300
 / PRIOR FILING DATE: 2002-09-17
 / NUMBER OF SEQ ID NOS: 32
 / SOFTWARE: PatentIn version 3.3
 / SEQ ID NO 1
 / LENGTH: 10
 / TYPE: PRT
 / ORGANISM: artificial sequence
 / FEATURE:
 / OTHER INFORMATION: TAT nuclear localization signal peptide
 / US-10-918-638-1

RESULT 3 US-10-246-300D-1
 / Sequence 1, Application US/10246300D
 / Publication No. US2006007434A1
 / GENERAL INFORMATION:
 / APPLICANT: Copharos
 / TITLE OF INVENTION: COBALAMIN MEDIATED DELIVERY OF NUCLEAR ACIDS, ANALOGS AND
 / FILE REFERENCE: COP1010
 / CURRENT APPLICATION NUMBER: US/10/246,300D
 / CURRENT FILING DATE: 2002-09-17
 / NUMBER OF SEQ ID NOS: 32
 / SOFTWARE: PatentIn version 3.3
 / SEQ ID NO 1
 / LENGTH: 10
 / TYPE: PRT
 / ORGANISM: artificial sequence
 / FEATURE:
 / OTHER INFORMATION: TAT nuclear localization signal peptide
 / US-10-246-300D-1

ALIGNMENTS

RESULT 1 US-0512-299A-45
 / Sequence 45, Application US/10512299A
 / Publication No. US20060057668A1
 / GENERAL INFORMATION:
 / APPLICANT: TOAGOSEI CO., LTD.
 / APPLICANT: YOSHIDA, Tetsuniko
 / APPLICANT: KUME, Masayoshi
 / APPLICANT: YAMADA, Hiroki
 / APPLICANT: KOURAI, Hiroki
 / TITLE OF INVENTION: ANTIMICROBIAL POLYPEPTIDE AND UTILIZATION THEREOF
 / FILE REFERENCE: 54003-8003 US00
 / CURRENT FILING DATE: 2004-10-21
 / PRIOR APPLICATION NUMBER: PCT/JP03/05225
 / PRIOR FILING DATE: 2003-04-24

RESULT 2 US-10-918-638-1
 / Sequence 1, Application US/10918638
 / Publication No. US20050249663A1
 / GENERAL INFORMATION:
 / APPLICANT: Copharos
 / TITLE OF INVENTION: COBALAMIN MEDIATED DELIVERY OF NUCLEAR ACIDS, ANALOGS
 / TITLE OF INVENTION: AND
 / TITLE OF INVENTION: DERIVATIVES THEREOF
 / FILE REFERENCE: COP1010
 / CURRENT APPLICATION NUMBER: US/10/918,638
 / CURRENT FILING DATE: 2004-08-12
 / PRIOR APPLICATION NUMBER: US/10/246,300
 / PRIOR FILING DATE: 2002-09-17
 / NUMBER OF SEQ ID NOS: 32
 / SOFTWARE: PatentIn version 3.3
 / SEQ ID NO 1
 / LENGTH: 10
 / TYPE: PRT
 / ORGANISM: artificial sequence
 / FEATURE:
 / OTHER INFORMATION: TAT nuclear localization signal peptide
 / US-10-918-638-1

RESULT 3 US-10-246-300D-1
 / Sequence 1, Application US/10246300D
 / Publication No. US2006007434A1
 / GENERAL INFORMATION:
 / APPLICANT: Copharos
 / TITLE OF INVENTION: COBALAMIN MEDIATED DELIVERY OF NUCLEAR ACIDS, ANALOGS AND
 / FILE REFERENCE: COP1010
 / CURRENT APPLICATION NUMBER: US/10/246,300D
 / CURRENT FILING DATE: 2002-09-17
 / NUMBER OF SEQ ID NOS: 32
 / SOFTWARE: PatentIn version 3.3
 / SEQ ID NO 1
 / LENGTH: 10
 / TYPE: PRT
 / ORGANISM: artificial sequence
 / FEATURE:
 / OTHER INFORMATION: TAT nuclear localization signal peptide
 / US-10-246-300D-1

US-11-179-639-21
 / Sequence 21, Application US/11179639
 / Publication No. US20060034805A1
 / GENERAL INFORMATION:
 / APPLICANT: FANG, JIANNIN
 / APPLICANT: JOOSS, KARIN
 / TITLE OF INVENTION: RAV VECTOR COMPOSITIONS AND METHODS FOR ENHANCED
 / EXPRESSION OF IMMUNOGLOBULINS USING THE SAME
 / FILE REFERENCE: 3802-101-11 US
 / CURRENT APPLICATION NUMBER: US/11/179, 639
 / CURRENT FILING DATE: 2005-07-13
 / PRIOR APPLICATION NUMBER: 60/587,082
 / PRIOR FILING DATE: 2004-07-13
 / SEQ ID NO: 21
 / LENGTH: 5
 / TYPE: PRT
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 / OTHER INFORMATION: peptide
 US-11-179-639-21

Query Match 83.3%; Score 25; DB 7; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRRKR 6
 Db 1 KRRKR 5

RESULT 9
 US-10-512-299A-55
 / Sequence 55, Application US/10512299A
 / Publication No. US20060057668A1
 / GENERAL INFORMATION:
 / APPLICANT: TOAGOSEI CO., LTD.
 / APPLICANT: YOSHIDA, Tetsuhiko
 / APPLICANT: KUME, Masayoshi
 / APPLICANT: KOURAI, Hiroki
 / TITLE OF INVENTION: ANTIMICROBIAL POLYPEPTIDE AND UTILIZATION THEREOF
 / FILE REFERENCE: 54003-8003.US00
 / CURRENT APPLICATION NUMBER: US/10/512,299A
 / CURRENT FILING DATE: 2004-10-21
 / PRIOR APPLICATION NUMBER: PCT/JP03/05225
 / PRIOR FILING DATE: 2003-04-24
 / PRIOR APPLICATION NUMBER: JP 2002-124830
 / PRIOR FILING DATE: 2002-04-25
 / NUMBER OF SEQ ID NOS: 123
 / SOFTWARE: Patentin version 3.3
 / SEQ ID NO: 55
 / LENGTH: 21
 / TYPE: PRT
 / ORGANISM: Rattus sp.
 US-10-512-299A-55

Query Match 83.3%; Score 25; DB 6; Length 21;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRKR 5
 Db 5 RKRKR 9

RESULT 10
 US-10-850-207-8
 / Sequence 8, Application US/10850207
 / Publication No. US2006028303A1
 / GENERAL INFORMATION:
 / APPLICANT: Spudich, James A.
 / APPLICANT: Nock, Steffen
 / APPLICANT: Wagner, Peter

RESULT 8
 US-11-242-243-8
 / Sequence 8, Application US/11242243
 / Publication No. US20060024805A1

/ TITLE OF INVENTION: Reversible Immobilization of Arginine-Tagged Moieties on a Silica Surface
 / TITLE OF INVENTION: Surface
 / FILE REFERENCE: UCSD-04726
 / CURRENT APPLICATION NUMBER: US/10/850,207
 / CURRENT FILING DATE: 2004-05-19
 / PRIORITY NUMBER: US/09/486,480
 / PRIOR FILING DATE: 2000-10-25
 / PRIOR APPLICATION NUMBER: PCT/US98/18531
 / PRIOR FILING DATE: 1998-09-03
 / PRIOR APPLICATION NUMBER: 80/057,929
 / PRIOR FILING DATE: 1997-09-04
 / NUMBER OF SEQ ID NOS: 9
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 8
 / LENGTH: 6
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Protein Transduction Domain
 / US-10-850-207-8

Query Match 80.0%; Score 24; DB 6; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.8e+05;
 Matches 4; Conservative 2; Mismatches 0;
 Indels 0; Gaps 0;
 Qy 1 RKRKR 6
 Db 1 RRRRR 6

RESULT 13
 US-11-107-371-6

/ Sequence 6, Application US/11107371
 / Publication No. US20060014289A1
 / GENERAL INFORMATION:
 / APPLICANT: AHMADIAN, MOHAMMAD
 / APPLICANT: CUI, KUNYUAN
 / APPLICANT: CHEN, LISHAN
 / APPLICANT: CHEN, SHU-CHIH
 / APPLICANT: HOUSTON JR, MICHAEL E.
 / TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING DELIVERY OF
 / TITLE OF INVENTION: DOUBLE-STRANDED RNA OR A DOUBLE-STRANDED HYBRID NUCLEIC
 / FILE REFERENCE: 04-02US
 / CURRENT APPLICATION NUMBER: US/11/107,371
 / CURRENT FILING DATE: 2005-04-15
 / PRIOR APPLICATION NUMBER: 60/564,543
 / PRIOR FILING DATE: 2004-04-20
 / NUMBER OF SEQ ID NOS: 21
 / SEQ ID NO 6
 / LENGTH: 7
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 / OTHER INFORMATION: Peptide
 / US-10-923-112A-44

Query Match 80.0%; Score 24; DB 6; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.8e+05;
 Matches 4; Conservative 2; Mismatches 0;
 Indels 0; Gaps 0;
 Qy 1 RKRKR 6
 Db 1 RRRRR 6

RESULT 11
 US-10-923-112A-44

/ Sequence 44, Application US/10923112A
 / Publication No. US20060040879A1
 / GENERAL INFORMATION:
 / APPLICANT: Kosak, Kenneth M.
 / TITLE OF INVENTION: Chloroquine Coupled Nucleic Acids and Methods for Their Synthesis
 / FILE REFERENCE: Confirmation No. 3293
 / CURRENT APPLICATION NUMBER: US/10/923,112A
 / CURRENT FILING DATE: 2004-08-21
 / NUMBER OF SEQ ID NOS: 54
 / SOFTWARE: PatentIn version 3.3
 / SEQ ID NO 44
 / LENGTH: 7
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Table I Transduction Peptide
 / US-10-923-112A-44

Query Match 80.0%; Score 24; DB 6; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.8e+05;
 Matches 4; Conservative 2; Mismatches 0;
 Indels 0; Gaps 0;
 Qy 1 RKRKR 6
 Db 1 RRRRR 6

RESULT 12
 US-11-041-103-5

/ Sequence 5, Application US/11041103
 / Publication No. US20050287518A1
 / GENERAL INFORMATION:
 / APPLICANT: Georgia Tech Research Corporation
 / APPLICANT: Bao, Gang
 / APPLICANT: Nitin, Nitin
 / FILE REFERENCE: 820701-1195
 / CURRENT APPLICATION NUMBER: US/11/041,103
 / CURRENT FILING DATE: 2005-01-21
 / PRIOR APPLICATION NUMBER: 10/179,730
 / PRIOR FILING DATE: 2002-06-25

Query Match 80.0%; Score 24; DB 7; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.8e+05;
 Matches 4; Conservative 2; Mismatches 0;
 Indels 0; Gaps 0;
 Qy 1 RKRKR 6
 Db 1 RRRRR 6

RESULT 14
 US-11-141-725-10

/ Sequence 10, Application US/11141725
 / Publication No. US20060014712A1
 / GENERAL INFORMATION:
 / APPLICANT: Neuman, Thomas
 / TITLE OF INVENTION: Controlled Delivery of Therapeutic Compounds
 / FILE REFERENCE: 34211/US/2 (473322-00024)

Query Match Score 24; DB 7; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.8e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRKR 6
 Db 1 :|||:
 1 RRRRRR 6

RESULT 21
 US-11-075-648A-8
 ; Sequence 8, Application US/11075648A
 ; Publication No. US20060030335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Healy, Judith M.
 ; APPLICANT: Kurz, Markus
 ; APPLICANT: McCauley, Thomas Greene
 ; APPLICANT: Thompson, Kristin
 ; APPLICANT: Wilson, Charles
 ; APPLICANT: Margolikes, Dorothy J.
 ; TITLE OF INVENTION: Controlled Modulation of the Pharmacokinetics and Biodistribution
 ; FILE REFERENCE: 23239-575
 ; CURRENT APPLICATION NUMBER: US/11/075,648A
 ; CURRENT FILING DATE: 2005-03-07
 ; PRIOR APPLICATION NUMBER: US 60/5550,790
 ; PRIOR FILING DATE: 2004-03-05
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO: 8
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic peptide

Query Match Score 24; DB 7; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.8e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRKR 6
 Db 1 :|||:
 1 RRRRRR 6

RESULT 22
 US-10-985-426-7
 ; Sequence 7, Application US/10985426
 ; Publication No. US20050256069A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Manoharan, Muthiah
 ; APPLICANT: Rajeev, Kallanthottathil G.
 ; TITLE OF INVENTION: RNA AGENTS WITH BIOCLEAVABLE TETHERS
 ; FILE REFERENCE: 14174-099001
 ; CURRENT APPLICATION NUMBER: US/10/985,426
 ; CURRENT FILING DATE: 2004-11-09
 ; PRIOR APPLICATION NUMBER: US 10/916,185
 ; PRIOR FILING DATE: 2004-08-11
 ; PRIOR APPLICATION NUMBER: PCT/US2004/011829
 ; PRIOR FILING DATE: 2004-04-16
 ; PRIOR APPLICATION NUMBER: US 60/465,665
 ; PRIOR FILING DATE: 2003-04-25
 ; PRIOR APPLICATION NUMBER: US 60/463,772
 ; PRIOR APPLICATION NUMBER: US 60/469,612
 ; PRIOR FILING DATE: 2003-05-09
 ; PRIOR APPLICATION NUMBER: US 60/465,802
 ; PRIOR FILING DATE: 2003-04-25
 ; PRIOR APPLICATION NUMBER: US 60/493,986
 ; PRIOR FILING DATE: 2003-08-08
 ; PRIOR APPLICATION NUMBER: US 60/494,597

; PRIOR FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: US 60/503,414
 ; PRIOR FILING DATE: 2003-05-15
 ; PRIOR APPLICATION NUMBER: US 60/506,341
 ; PRIOR FILING DATE: 2003-09-26
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: FastSeqQ for Windows Version 4.0
 ; SEQ ID NO: 7
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Exemplary Cell Permeation Peptide

US-10-985-426-7

Query Match Score 24; DB 6; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.8e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRKR 6
 Db 1 :|||:
 1 RRRRRR 6

RESULT 23
 US-10-509-787A-140
 ; Sequence 140, Application US/10509787A
 ; Publication No. US20050287602A1
 ; GENERAL INFORMATION:
 ; APPLICANT: O'DOWD, BRIAN F.
 ; APPLICANT: GEORGE, SUSAN R.
 ; TITLE OF INVENTION: METHOD OF IDENTIFYING TRANSMEMBRANE PROTEIN-INTERACTING COMPOUNDS
 ; FILE REFERENCE: 3477-110
 ; CURRENT APPLICATION NUMBER: US/10/509,787A
 ; CURRENT FILING DATE: 2004-09-30
 ; PRIOR APPLICATION NUMBER: PCT/CA03/00542
 ; PRIOR FILING DATE: 2003-04-11
 ; PRIOR APPLICATION NUMBER: 60/442,556
 ; PRIOR FILING DATE: 2003-01-27
 ; PRIOR APPLICATION NUMBER: 60/422,891
 ; PRIOR FILING DATE: 2002-11-01
 ; PRIOR APPLICATION NUMBER: 60/387,570
 ; PRIOR FILING DATE: 2002-06-12
 ; PRIOR APPLICATION NUMBER: 60/379,419
 ; PRIOR FILING DATE: 2002-05-13
 ; PRIOR APPLICATION NUMBER: 60/371,704
 ; NUMBER OF SEQ ID NOS: 158
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 140
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthesized

US-10-509-787A-140

Query Match Score 24; DB 6; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.8e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRKR 6
 Db 2 :|||:
 2 KKKKKR 7

RESULT 24
 US-10-512-299A-12
 ; Sequence 12, Application US/10512299A
 ; Publication No. US2006005768A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TOAGOSEI CO., LTD.

APPLICANT: YOSHIDA, Tetsuhiko ; APPLICANT: KUME, Masayoshi ; APPLICANT: YAMADA, Yoshinao ; APPLICANT: KOURAI, Hiroki ; TITLE OF INVENTION: ANTIMICROBIAL POLYPEPTIDE AND UTILIZATION THEREOF ; FILE REFERENCE: 54003 8003 US00 ; CURRENT APPLICATION NUMBER: US/10/512,299A ; CURRENT FILING DATE: 2004-10-21 ; PRIOR APPLICATION NUMBER: PCT/JP03/05225 ; PRIOR FILING DATE: 2003-04-24 ; PRIOR APPLICATION NUMBER: JP 2002-124830 ; PRIOR FILING DATE: 2002-04-25 ; NUMBER OF SEQ ID NOS: 123 ; SEQ ID NO 12 ; SOFTWARE: PatentIn version 3.3 ; LENGTH: 9 ; ORGANISM: Drosophila sp. ; SEQ ID NO 12-299A-12

Query Match 80.0%; Score 24; DB 6; Length 9; Best Local Similarity 66.7%; Pred. No. 1.8e+05; Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0; SEQ ID NO 47

Qy 1 RKRKR 6 :|:|:| Db 2 EKKERKR 7

RESULT 25 US-11-016-542-20

Sequence 20, Application US/11016542 ; Publication No. US2005282239A1 ; GENERAL INFORMATION: ; APPLICANT: ALLBRITTON, NANCY L. ; SIMS, CHRISTOPHER E. ; APPLICANT: ROSSI, FRANCIS M. ; APPLICANT: SOUGHAYER, JOSEPH S. ; TITLE OF INVENTION: A CELL-PERMEABLE ENZYME ACTIVATION REPORTER THAT CAN BE TITLE OF INVENTION: LOADED IN A HIGH THROUGHPUT AND GENTLE MANNER ; CURRENT APPLICATION NUMBER: US/11/016,542 ; FILE REFERENCE: CAL02-003-US ; CURRENT FILING DATE: 2004-12-17 ; PRIOR APPLICATION NUMBER: 60/530,875 ; PRIOR FILING DATE: 2003-12-17 ; NUMBER OF SEQ ID NOS: 20 ; SOFTWARE: PatentIn Ver. 3.3 ; SEQ ID NO 20 ; LENGTH: 9 ; TYPE: PRT ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide ; OTHER INFORMATION: Peptide

Query Match 80.0%; Score 24; DB 7; Length 9; Best Local Similarity 66.7%; Pred. No. 1.8e+05; Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0; SEQ ID NO 20

Qy 1 RKRKR 6 :|:|:| Db 1 EKKERKR 7

RESULT 26 US-11-133-804-47

Sequence 47, Application US/11133804 ; Publication No. US2006041105A1 ; GENERAL INFORMATION: ; APPLICANT: Jiang, Tao ; Olsen, Emilia S. ; Whitney, Michael ; APPLICANT: Tsien, Roger Y. ; APPLICANT: The Regents of the University of California ; TITLE OF INVENTION: Peptides Whose Uptake by Cells is Controllable

APPLICANT: YOSHIDA, Tetsuhiko ; APPLICANT: KUME, Masayoshi ; APPLICANT: YAMADA, Yoshinao ; APPLICANT: KOURAI, Hiroki ; TITLE OF INVENTION: ANTIMICROBIAL POLYPEPTIDE AND UTILIZATION THEREOF ; FILE REFERENCE: 023078-161520US ; CURRENT APPLICATION NUMBER: US/11/133,804 ; CURRENT FILING DATE: 2005-05-19 ; PRIOR APPLICATION NUMBER: US 10/699,562 ; PRIOR FILING DATE: 2003-10-31 ; NUMBER OF SEQ ID NOS: 85 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 47 ; LENGTH: 9 ; TYPE: PRT ; FEATURE: ; ORGANISM: Artificial Sequence ; OTHER INFORMATION: Description of Artificial Sequence: amino acid sequence ; OTHER INFORMATION: Portion of compound (f) of Figure 17, R9, Arg9, ; OTHER INFORMATION: Peptide portion B, uptake sequence US-11-133-804-47

Query Match 80.0%; Score 24; DB 7; Length 9; Best Local Similarity 66.7%; Pred. No. 1.8e+05; Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0; SEQ ID NO 47

Qy 1 RKRKR 6 :|:|:| Db 1 EKKERKR 7

RESULT 27 US-11-200-703-7

Sequence 7, Application US/11200703 ; Publication No. US2006005826A1 ; GENERAL INFORMATION: ; APPLICANT: Manoharan, Muthiah ; APPLICANT: Kesavar, Venkatachali G. ; APPLICANT: Rajeev, Kallanthottathil G. ; TITLE OF INVENTION: CHEMICALY MODIFIED OLIGONUCLEOTIDES ; FILE REFERENCE: 14174-089001 ; CURRENT APPLICATION NUMBER: US/11/200,703 ; CURRENT FILING DATE: 2005-08-10 ; PRIOR APPLICATION NUMBER: 60/600,703 ; PRIOR FILING DATE: 2004-08-10 ; NUMBER OF SEQ ID NOS: 106 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 7 ; LENGTH: 9 ; TYPE: PRT ; FEATURE: ; OTHER INFORMATION: Exemplary Cell Permeation Peptide

Query Match 80.0%; Score 24; DB 7; Length 9; Best Local Similarity 66.7%; Pred. No. 1.8e+05; Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0; SEQ ID NO 7

Qy 1 RKRKR 6 :|:|:| Db 1 EKKERKR 7

RESULT 28 US-11-133-804-85

Sequence 85, Application US/11133804 ; Publication No. US2006041105A1 ; GENERAL INFORMATION: ; APPLICANT: Jiang, Tao ; Olsen, Emilia S. ; Whitney, Michael ; APPLICANT: Tsien, Roger Y. ; APPLICANT: The Regents of the University of California ; TITLE OF INVENTION: Peptides Whose Uptake by Cells is Controllable

APPLICANT: YOSHIDA, Tetsuhiko ; APPLICANT: KUME, Masayoshi ; APPLICANT: YAMADA, Yoshinao ; APPLICANT: KOURAI, Hiroki ; TITLE OF INVENTION: ANTIMICROBIAL POLYPEPTIDE AND UTILIZATION THEREOF ; FILE REFERENCE: 023078-161520US ; CURRENT APPLICATION NUMBER: US/11/133,804 ; CURRENT FILING DATE: 2005-05-19 ; PRIOR APPLICATION NUMBER: US 10/699,562 ; PRIOR FILING DATE: 2003-10-31 ; NUMBER OF SEQ ID NOS: 85 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 47 ; LENGTH: 9 ; TYPE: PRT ; FEATURE: ; ORGANISM: Artificial Sequence ; OTHER INFORMATION: Description of Artificial Sequence: amino acid sequence ; OTHER INFORMATION: Portion of compound (f) of Figure 17, R9, Arg9, ; OTHER INFORMATION: Peptide portion B, uptake sequence US-11-133-804-85

Query Match 80.0%; Score 24; DB 7; Length 9; Best Local Similarity 66.7%; Pred. No. 1.8e+05; Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0; SEQ ID NO 47

Qy 1 RKRKR 6 :|:|:| Db 1 EKKERKR 7

```

; FILE REFERENCE: 02307E-161520US
; CURRENT APPLICATION NUMBER: US/11/133,804
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US 10/699,562
; PRIOR FILING DATE: 2003-10-31
; SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 85
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:basic portion B
; NAME/KEY: MOD_RES
; LOCATION: (1)__
; OTHER INFORMATION: Xaa = lysinamide attached through alpha and
; OTHER INFORMATION: epsilon nitrogen-bound cargo molecule
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)_
; OTHER INFORMATION: Xaa = dodecaheptyl-arginine
; US-11-133-804-85

Query Match Score 24; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKRKRKR 6
Db 2 RRRRRR 7

```

```

RESULT 29
US-10-535-780-3
; Sequence 3, Application US/10535780
; Publication No. US20060026718A1
; GENERAL INFORMATION:
; APPLICANT: Werner, Stefan
; APPLICANT: Marillonet, Sylvestre
; APPLICANT: Klimyuk, Victor
; APPLICANT: Gleba, Yuri
; TITLE OF INVENTION: Method of Controlling Cellular Processes in Plants
; FILE REFERENCE: 049202/289227
; CURRENT APPLICATION NUMBER: US/10/535,780
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: PCT/EP03/13018
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: DE 102 54 166.3
; PRIOR FILING DATE: 2002-11-20
; SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Membrane Translocation Signal
; US-10-535-780-3

Query Match Score 24; DB 6; Length 11;
Best Local Similarity 66.7%; Pred. No. 50;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 RKRKRKR 6
Db 1 RRRRRR 6
; RESULT 30
; US-10-955-739-6
; Sequence 6, Application US/10955739
; Publication No. US20060067925A1

```

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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 13, 2006, 08:45:30 ; Search time 38 Seconds
(without alignments)
15.192 Million cell updates/sec

Title: US-09-816-688B-1
Perfect score: 30
Sequence: 1 RKKRR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4071

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 150 summaries

Database : PIR 80.4*
1: pir1:*,
2: pir2:*,
3: pir3:*,
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	83.3	21	2 ISB423	arylhdrocarbon re transcription fact
2	22	73.3	10	2 A22089	platelet-derived g
3	22	73.3	18	2 PS0387	sperm chromatin pr
4	22	73.3	21	2 PN0082	ribosomal protein
5	21	70.0	16	2 A28144	pyrB leader peptid
6	20	66.7	19	2 B39845	histone H1 - sea u
7	20	66.7	21	2 PS0146	caraspin - golifis
8	20	66.7	21	2 JH0161	caldesmon - turkey
9	18	60.0	16	2 A5552	lactose phosphotra
10	17	56.7	13	2 B39778	glycogen phosphory
11	17	56.7	14	2 PL0040	CAMP-regulated pho
12	17	56.7	19	2 A33361	MHC HLA-DR gamma C
13	17	56.7	20	2 IS5563	probable nitrate r
14	17	56.7	21	2 S61306	Ca2+-transporting
15	16	53.3	8	2 161832	ribosomal protein
16	16	53.3	9	2 S78762	NADH2 dehydrogenas
17	16	53.3	10	2 PQ0785	lamin B receptor -
18	16	53.3	16	2 A27803	spermadhesin AWW h
19	16	53.3	16	2 S05703	ribosomal protein
20	16	53.3	18	2 S55270	GATA-2 protein - A
21	16	53.3	19	4 151264	rhodopsin single b
22	16	53.3	20	2 S00315	photosystem I chl
23	16	53.3	20	2 S28405	lamin B receptor -
24	15	50.0	14	2 S51426	spermadhesin AWW h
25	15	50.0	15	2 S16888	ribosomal protein
26	15	50.0	15	2 S216891	vespulakinin 1 - e
27	15	50.0	17	1 A61339	transglutaminase
28	15	50.0	18	2 S45373	monocyte chemotact
29	15	50.0	20	2 I67551	valine-tRNA ligase

30	14	46.7	2 PC7076
31	14	46.7	10 F41839
32	14	46.7	11 J00395
33	14	46.7	11 PH0919
34	14	46.7	12 A40763
35	14	46.7	12 S29859
36	14	46.7	13 JH0460
37	14	46.7	14 PC1215
38	14	46.7	14 ribosomal protein B
39	14	46.7	15 C48401
40	14	46.7	15 T-cell receptor be
41	14	46.7	15 ribosomal protein
42	14	46.7	15 heparin-binding le
43	14	46.7	16 orf 61.1 - phage T
44	14	46.7	17 hypothetical prote
45	14	46.7	18 interleukin-7 rece
46	14	46.7	18 epsilon receptor m
47	14	46.7	20 flavodoxin B - Azo
48	14	46.7	20 histone H4 - sea u
49	14	46.7	20 ribosomal protein
50	14	46.7	21 30K serine protein
51	13	43.3	10 matrix metallopro
52	13	43.3	12 Ig H chain V-D-J r
53	13	43.3	13 ribosomal protein
54	13	43.3	13 argA protein - Sal
55	13	43.3	13 ribosomal protein
56	13	43.3	14 chaperone, TCP1-re
57	13	43.3	14 probursin tetradec
58	13	43.3	15 placental calcium
59	13	43.3	15 32K variable histio
60	13	43.3	15 urogenital tumor m
61	13	43.3	15 casein kinase II -
62	13	43.3	16 aldehyde dehydroge
63	13	43.3	16 homeotic protein G
64	13	43.3	18 acrosin (EC 3.4.1)
65	13	43.3	18 translation elonga
66	13	43.3	18 21K high mobility
67	13	43.3	19 21K high mobility
68	13	43.3	19 21K high mobility
69	13	43.3	20 1lysozyme (EC 3.2.1
70	13	43.3	20 15K protein B - ra
71	13	43.3	20 S02175
72	13	43.3	20 S32387
73	13	43.3	20 H+-exporting ATPa
74	13	43.3	21 dehydrin 7.5K pol
75	12	40.0	4 phospholipase C (B
76	12	40.0	7 ribosomal protein
77	12	40.0	8 element, P cycot
78	12	40.0	8 PT0323
79	12	40.0	10 gene B-50 protein
80	12	40.0	11 152645
81	12	40.0	11 pyrE leader peptid
82	12	40.0	12 LPECP8
83	12	40.0	13 neurotensin - gln
84	12	40.0	14 19 kappa chain J S
85	12	40.0	14 25K elastin-bindin
86	12	40.0	14 28R protein
87	12	40.0	15 2A5417
88	12	40.0	15 2A56835
89	12	40.0	15 2A56835
90	12	40.0	15 2A56835
91	12	40.0	17 2A56835
92	12	40.0	17 2A56835
93	12	40.0	17 2A27636
94	12	40.0	17 2A38824
95	12	40.0	17 2JX0125
96	12	40.0	17 2C84063
97	12	40.0	18 2S56715
98	12	40.0	18 2PH1621
99	12	40.0	18 2JU0124
100	12	40.0	18 2JU0125
101	12	40.0	19 2PC13225
102	12	40.0	19 2A49725

A; Cross-references: UNIPARC:UPI0001764FC
A; Note: This protein corresponds to the Gloma type of human A chain
C; Superfamily: platelet-derived growth factor

```

SUTT 1
8443
Squalylhydrocarbon receptor - mouse
Species: Mus sp. (mouse)
Accession: I58423
Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
QY
2 KRRKR 6
|:|||:|

```

A;Molecule type: protein
 A;Residues: 1-21 <OSA>
 A;Cross-references: UNIPROT:Q7M3Z3; UNIPARC:UPI00001771FA
 A;Experimental source: sperm
 C;Superfamily: sperm histone
 C;Keywords: sperm

Query Match 73.3%; Score 22; DB 2; Length 21;
 Best Local Similarity 66.7%; Pred. No. 4.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RKKRKR 6
 Db 2 RRRRSR 7

RESULT 5

A28144
 ribosomal protein S27a - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 09-Jul-2004
 C;Accession: A28144
 R;Reedman, K.L.; Rechsteiner, M.
 J.; Biol. Chem. 263, 4926-4931, 1988
 A;Title: Extended reading frame of a ubiquitin gene encodes a stable, conserved, basic protein
 A;Reference number: A28144; MUID:88169619; PMID:2832412
 A;Accession: A28144
 A;Molecule type: protein
 A;Residues: 1-16 <REBD>
 A;Cross-references: UNIPROT:O97577; UNIPARC:UPI0000177161
 C;Superfamily: ubiquitin / rat ribosomal protein S27a; ribosomal protein S27a homology;
 C;Keywords: protein biosynthesis

Query Match 70.0%; Score 21; DB 2; Length 16;
 Best Local Similarity 50.0%; Pred. No. 5.8e+02;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RKKRKR 6
 Db 2 RRRKKK 7

RESULT 6

B39845
 PYRB leader peptide - *Bacillus subtilis*
 C;Species: *Bacillus subtilis*
 C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 05-Oct-2004
 C;Accession: B39845
 R;Quinn, C.L.; Stephenson, B.T.; Switzer, R.L.
 J.; Biol. Chem. 266, 913-9127, 1991
 A;Title: Functional organization and nucleotide sequence of the *Bacillus subtilis* Pyrimidine operon
 A;Reference number: A39845; MUID:91225016; PMID:1709162
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-19 <QUI>
 A;Cross-references: UNIPARC:UPI000017A35G; GB: M59757

Query Match 66.7%; Score 20; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 KRRK 5
 Db 2 KRRK 5

RESULT 7

PS0146
 histone H1 - sea urchin (*Hemicentrotus pulcherrimus*) (fragment)
 C;Species: *Hemicentrotus pulcherrimus*
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
 C;Accession: PS0146

R;Suzuki, M.; Sugiyama, M.; Ebashi, S.
 J. Biochem. 108, 341-355, 1990
 A;Title: Sea urchin protease specific to the SPKK motif in histone.
 A;Reference number: PS0145; MUID:9115778; PMID:2126010
 A;Accession: PS0146
 A;Molecule type: protein
 A;Residues: 1-21 <SPKK>
 A;Cross-references: UNIPROT:Q7M3M1; UNIPARC:UPI000017BP14
 C;Keywords: chromosomal protein; nucleosome

Query Match 66.7%; Score 20; DB 2; Length 21;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RKRKRK 5
 Db 13 RSRRK 17

RESULT 8

JH0361
 carassin - goldfish
 N;Alternative names: tachykinin-related peptide
 C;Species: *Carassius auratus* (goldfish)
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
 C;Accession: JH0361
 R;Conlon, J.M.; O'Harte, F.; Peter, R.E.; Kah, O.
 J. Neurochem. 56, 1432-1436, 1991
 A;Title: Carassin: a tachykinin that is structurally related to neuropeptide-gamma from teleost fish
 A;Reference number: JH0361; MUID:91162221; PMID:202352
 A;Accession: JH0361
 A;Molecule type: protein
 A;Residues: 1-21 <CON>
 A;Cross-references: UNIPROT:PP5421; UNIPARC:UPI0000136FDE
 A;Experimental source: brain
 C;Keywords: amidated carboxyl end
 P;21/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 66.7%; Score 20; DB 2; Length 21;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 66.7%; Score 20; DB 2; Length 21;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 9

A35552
 caldeom - turkey (fragment)
 C;Species: *Meleagris gallopavo* (common turkey)
 C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 09-Jul-2004
 R;Velaz, D.; Ingram, R.H.; Chalovich, J.M.
 J. Biol. Chem. 265, 2929-2934, 1990
 A;Title: Dissociation of the effect of caldeom on the ATPase activity and on the bindir A;Accession: A35552
 A;Reference number: A35552; MUID:90153946; PMID:2137453
 A;Accession: A35552
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-16 <VPL>
 A;Cross-references: UNIPROT:Q7LZ12; UNIPARC:UPI000017C045

Query Match 60.0%; Score 18; DB 2; Length 16;
 Best Local Similarity 60.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Query 2 KRRKR 6
 Db 10 RRQKR 14

RESULT 10

E39778 lactose phosphotransferase system lacR protein - *Lactococcus lactis* (fragment)
 C;Species: *Lactococcus lactis*
 C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 09-Jul-2004
 C;Accession: E39778
 R;van Rooijen, R.J.; van Schalkwijk, S.; de Vos, W.M.
 J. Biol. Chem. 266, 7176-7181, 1991.
 A;Title: Molecular cloning, characterization, and nucleotide sequence of the tagatose 6-
 A;Reference: A39778; MUID:91201377; PMID:1901863
 A;Accession: E39778
 A;Status: preliminary
 A;Keywords: DNA binding; transcription regulation
 C;Cross-references: UNIPROT:PI08016; UNIPARC:UPI00001787DC; GB:J05748
 C;Superfamily: regulatory protein gntR
 C;Keywords: DNA binding; transcription regulation

Query Match 56.7%; Score 17; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRRR 4
 Db 9 KRRR 12

RESULT 11
 PL0040 glycogen phosphorylase (EC 2.4.1.1), cardiac - pig (fragment)
 C;Species: *Sus scrofa domestica* (domestic pig)
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 A;Accession: PL0040
 R;Dobbradi, V.; Willis, A.C.; Verbi, G.; Johnson, L.N.
 Comp. Biochem. Physiol. B 91, 717-721, 1988.
 A;Title: The sequence around the phosphorylation site of the porcine heart type phospho-
 A;Reference: PL0040; MUID:89136523; PMID:3224509
 A;Accession: PL0040
 A;Molecule type: protein
 A;Residues: 1-14 <DOM>
 A;Cross-references: UNIPROT:Q7M385; UNIPARC:UPI000017045F
 A;Experimental source: heart
 C;Keywords: allosteric regulation; cardiac muscle; glycogen metabolism; glycosyltransferase;
 F10;Binding site: phosphatase (Ser) (covalent) #status experimental

Query Match 56.7%; Score 17; DB 2; Length 14;
 Best Local Similarity 60.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRRR 6
 Db 4 ERKQ 8

RESULT 12
 A33361 cAMP-regulated phosphoprotein, 21k - rat (fragment)
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 09-Jul-2004
 C;Accession: A33361
 R;Hammons Jr., H.C.; Girault, J.A.; Williams, K.R.; IoPresti, M.B.; Greengard, P.
 J. Biol. Chem. 264, 7726-7733, 1989.
 A;Title: ARPP-21, a cyclic AMP-regulated phosphoprotein (M-r=21,000) enriched in dopaminergic studies of its phosphorylation in vitro.
 A;Reference number: A33361; MUID:89214228; PMID:2540203
 A;Accession: A33361
 A;Molecule type: protein
 A;Residues: 1-19 <HIM>
 A;Cross-references: UNIPROT:Q7M049; UNIPARC:UPI00001769D7
 C;Keywords: phosphoprotein

Query Match 56.7%; Score 17; DB 2; Length 19;
 Best Local Similarity 60.0%; Pred. No. 3.2e+03;

Matches 3; Conservative 2; Mismatches 0;
 Qy 1 KRRK 5
 Db 5 QERRK 9

RESULT 13
 I55663 MHC HLA-DR gamma chain - human (fragment)
 C;Species: *Homo sapiens* (man)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C;Accession: I55663
 R;O'Sullivan, D.M.; Noonan, D.; Quaranta, V.
 J. Exp. Med. 166, 444-450, 1987
 A;Title: Four Ia invariant chain forms derive from a single gene by alternate splicing at
 A;Reference number: I55663; MUID:87252940; PMID:3036398
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-20 <RBS>
 A;Cross-references: UNIPROT:019685; UNIPARC:UPI0000895C2; GB:M28588; NID:9292150; PIDN:1
 C;Genetics:
 A;Gene: HLA-DR

Query Match 56.7%; Score 17; DB 2; Length 20;
 Best Local Similarity 60.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KRRR 6
 Db 3 RRRSR 7

RESULT 14
 S61306 probable nitrate reductase alpha chain - *Thiobacillus pantotropha* (fragment)
 C;Species: *Thiobacillus pantotropha*
 C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
 C;Accession: S61306
 R;Berks, B.C.; Page, M.D.; Richardson, D.J.; Reilly, A.; Cavill, A.; Outer, F.; Ferguson, Nol. Microbiol. 15, 319-331, 1995
 A;Title: Sequence analysis of subunits of the membrane-bound nitrate reductase from a delta
 f a redox loop.
 A;Reference number: S61306; MUID:95264918; PMID:7746153
 A;Accession: S61306
 A;Cross-references: UNIPARC:UPI00000B21EE; EMBL:226255; NID:9541760; PIDN:CAA81214; PII
 A;Note: The nucleotide sequence was submitted to the EMBL Data Library, September 1994
 C;Genetics:
 A;Gene: narG
 C;Keywords: membrane-associated complex

Query Match 56.7%; Score 17; DB 2; Length 21;
 Best Local Similarity 75.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRRR 5
 Db 15 KRRR 18

RESULT 15
 I64832 Ca2+-transporting ATPase (EC 3.6.3.8) - rat (fragment)
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 02-Aug-1995 #sequence_revision 02-Aug-1995 #text_change 09-Jul-2004
 C;Accession: I64832
 R;Wu, K.
 Am. J. Physiol. 264, 333-341, 1993
 A;Title: Molecular cloning and quantification of mRNA and protein encoding Ca2+-ATPase in

A;Reference number: I51892
 A;Accession: 164832
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-8 <RES>
 A;Cross-references: UNIPROT:Q63139; UNIPARC:UPI00001708F8; GB:MM99223; NID:9203644; PIDN:
 C;Genetics:
 C;Keywords: hydrolase

RESULT 18
 A;Accession: A27803
 A;Status: myosin light chain, smooth muscle - turkey (fragment)
 C;Species: *Meleagris gallopavo* (common turkey)
 C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 09-Jul-2004
 R:Bengur, A.R.; Robinson, B.A.; Appella, E.; Sellers, J.R.
 C;Accession: A27803
 A;Title: Sequence of the sites phosphorylated by protein kinase C in the smooth muscle m₃
 A;Reference number: A27803; MUID:8722230; PMID:3584131
 A;Accession: A27803
 A;Molecule type: protein
 A;Residues: 1-16 <BRN>
 A;Cross-references: UNIPROT:Q1LZ79; UNIPARC:UPI00001776B1
 C;Superfamily: calmodulin; calmodulin repeat homology
 C;Keywords: EF hand; muscle; smooth muscle

Query Match 53.3%; Score 16; DB 2; Length 16;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 KRRK 5
 Db 5 ERK 8

Query Match 53.3%; Score 16; DB 2; Length 16;
 Best Local Similarity 50.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RKRKR 6
 Db 11 KRPQPR 16

RESULT 19
 A;Accession: S05703
 A;Status: homeotic protein ceh-2 - *Caenorhabditis elegans* (fragment)
 C;Species: *Caenorhabditis elegans*
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 05-Oct-2004
 C;Accession: S05703
 R:Buerlin, T.R.; Finney, M.; Coulson, A.; Ruvkun, G.
 Nature 341, 239-243, 1989
 A;Title: *Caenorhabditis elegans* has scores of homeobox-containing genes.
 A;Reference number: S05703; MUID:89384901; PMID:2571091
 A;Status: not compared with conceptual translation
 A;Accession: S05703
 A;Molecule type: DNA
 A;Residues: 1-16

 A;Cross-references: UNIPROT:001962; UNIPARC:UPI000017A2EF
 C;Genetics:
 A;Gene: ceh-2
 A;Map position: 1
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 53.3%; Score 16; DB 2; Length 16;
 Best Local Similarity 50.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 RKRKR 6
 Db 9 RTKHKR 14

RESULT 20
 A;Accession: S54270
 A;Status: GATA-2 protein - African clawed frog
 C;Species: *Xenopus laevis* (African clawed frog)
 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 R:Brewer, A.C.; Guille, M.J.; Fear, D.J.; Partington, G.A.; Patient, R.K.
 BMBO J. 11, 75-766, 1995
 A;Title: Nuclear translocation of a maternal CCAAT factor at the start of gastrulation ac_{ac}
 A;Reference number: S54270
 A;Molecule type: DNA
 A;Residues: 1-18

 A;Cross-references: UNIPROT:Q7LZS3; UNIPARC:UPI000017BF91

Query Match 53.3%; Score 16; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RKRK 5
 Db 6 QKERK 10

RESULT 16
 A;Accession: S78762
 A;Status: ribosomal protein MRP-S12, mitochondrial - bovine (fragment)
 C;Species: *Bos primigenius taurus* (cattle)
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C;Accession: S78762
 R;Grack, H.R.
 submitted to the Protein Sequence Database, July 1999
 A;Reference number: S78760
 A;Accession: S78762
 A;Molecule type: protein
 A;Residues: 1-9 <GRA>
 C;Keywords: mitochondrial
 C;Cross-references: UNIPROT:Q7M375; UNIPARC:UPI000017C56B
 P;1-9/Product: ribosomal protein MRP-S12 (fragment) #status experimental <MAT>

Query Match 53.3%; Score 16; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 RKRKR 6
 Db 3 RKRVRPR 8

RESULT 17
 A;Accession: P00785
 A;Status: NADH dehydrogenase (BC 1.6.99.3) 27K chain - fava bean mitochondrial (fragment)
 N;Alternate names: complex I 27K chain; NADH:ubiquinone reductase 27K chain
 C;Species: mitochondrial Vicia faba (fava bean)
 C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
 C;Accession: P00785
 R;Letertre, S.; Bouthry, M.
 Plant Physiol. 102, 435-443, 1993
 A;Title: Purification and preliminary characterization of mitochondrial complex I (NADH:
 A;Reference number: P00785; MUID:94151437; PMID:8108509
 A;Accession: P00785
 A;Molecule type: protein
 A;Residues: 1-10 <LET>
 A;Cross-references: UNIPROT:Q7M2G2; UNIPARC:UPI000017CD49
 C;Comment: Complex I, mitochondrial NADH:ubiquinone reductase, is the first of the three
 C;Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by
 C;Genetics:
 A;Genome: mitochondrial
 C;Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 53.3%; Score 16; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RKRK 5
 Db 6 QKERK 10

Query Match Similarity 53.3%; Score 16; DB 2; Length 18;
 Best Local Similarity 75.0%; Pred. No. 4.5e-03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

R;Simos, G.; Georgatos, S.D.
 EMBO J. 11, 4077-4036, 1992
 A;Title: The inner nuclear membrane protein p58 associates in vivo with a p58 kinase and
 A;Reference number: S28405; PMID:93010598; MUID:1327755
 A;Accession: S28405
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <SM>
 A;Cross-references: UNIPROT:Q1L211; UNIPARC:UPI000017C046
 C;Keywords: DNA binding; nucleus; receptor; transmembrane protein

RESULT 21
 I54264 rhodopsin single base deletion frame shift mutant - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 02-Jul-1996 #sequence_revision 08-Nov-1996 #text_change 20-Apr-2000
 R;Horn, M.; Humphries, P.; Kunisch, M.; Marchese, C.; Apfelstedt-Sylla, B.; Fugi, L.; Zr
 Hum. Genet. 90, 255-257, 1992
 A;Title: Deletions in exon 5 of the human rhodopsin gene causing a shift in the reading
 A;Reference number: I54264; MUID:93138610; PMID:1487240
 A;Accession: I54264
 A;Molecule type: DNA
 A;Residues: 1-19 <HOR>
 A;Cross-references: UNIPARC:UPI000011DDF9; GB:SS558443; NID:9266287; PID:AB25673.1; PID:
 A;Genetics: A;Gene: GDB:RH0
 A;Cross-references: GDB:120347
 A;Map position: 3q21.3-3q24
 Query Match Similarity 53.3%; Score 16; DB 4; Length 19;
 Best Local Similarity 60.0%; Pred. No. 4.7e-03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KRRKR 6
 Db 1 RRRAR 5

RESULT 22
 S00315 photosystem I chain III - garden pea (fragment)
 N;Alternate names: photosystem I
 C;Species: Pisum sativum (garden pea)
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C;Accession: S00315; P00118
 R;Dunn, P.P.J.; Packman, L.C.; Pappin, D.; Gray, J.C.
 FEBS Lett. 228, 157-161, 1988
 A;Title: N-terminal amino acid sequence analysis of the subunits of pea photosystem I.
 A;Reference number: S00314; MUID:88137587; PMID:3277857
 A;Accession: S00315
 A;Molecule type: protein
 A;Residues: 1-20 <DN>
 A;Cross-references: UNIPROT:P20119; UNIPARC:UPI0000132517
 A;Note: 1-Asp was also found
 C;Superfamily: photosystem I chain III
 C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid
 Query Match Similarity 53.3%; Score 16; DB 2; Length 20;
 Best Local Similarity 60.0%; Pred. No. 4.9e-03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KRRKR 6
 Db 16 KREKQ 20

RESULT 23
 S28405 lamin B receptor - turkey (fragment)
 N;Alternate names: inner nuclear membrane protein p58
 C;Species: Meleagris gallopavo (common turkey)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S28405

R;Simos, G.; Georgatos, S.D.
 EMBO J. 11, 4077-4036, 1992
 A;Title: The inner nuclear membrane protein p58 associates in vivo with a p58 kinase and
 A;Reference number: S28405; PMID:93010598; MUID:1327755
 A;Accession: S28405
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <SM>
 A;Cross-references: UNIPROT:Q1L211; UNIPARC:UPI000017C046
 C;Keywords: DNA binding; nucleus; receptor; transmembrane protein

Query Match Similarity 53.3%; Score 16; DB 2; Length 20;
 Best Local Similarity 75.0%; Pred. No. 4.9e-03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRRK 5
 Db 1 KQRK 4

RESULT 24
 S58426 permadheuin AWN homolog - horse (fragment)
 C;Species: Equus caballus (domestic horse)
 C;Date: 12-Feb-1998 #sequence_revision 15-May-1998 #text_change 07-May-1999
 C;Accession: S58426
 R;Calvete, J.J.; Mann, K.; Schaefer, W.; Sanz, I.; Reinert, M.; Nessau, S.; Raida, M.; Tr
 Biochem. J. 310, 615-622, 1995
 A;Title: Amino acid sequence of HSP-1, a major protein of stallion seminal plasma: effect
 A;Reference number: S58424; PMID:95382782; PMID:7654203
 A;Accession: S58426
 A;Molecule type: protein
 A;Residues: 1-14 <CAL>
 A;Cross-references: UNIPARC:UPI000017C44B
 A;Experimental source: seminal plasma

Query Match Similarity 50.0%; Score 15; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 5.5e-03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RRKR 6
 Db 4 RRSR 7

RESULT 25
 S36888 ribosomal protein S12 - Mycobacterium bovis (fragment)
 C;Species: Mycobacterium bovis
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S36888
 R;Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
 FEBS Lett. 331, 9-14, 1993
 A;Title: Isolation and amino acid sequence of the 30S ribosomal protein S12
 A;Reference number: S36887; PMID:9409653; PMID:8405418
 A;Accession: S36888
 A;Molecule type: protein
 A;Residues: 1-15 <OBA>
 A;Cross-references: UNIPROT:Q53538; UNIPARC:UPI000017729F
 C;Superfamily: ribosomal protein S12
 C;Keywords: protein biosynthesis; ribosome

Query Match Similarity 50.0%; Score 15; DB 2; Length 15;
 Best Local Similarity 60.0%; Pred. No. 5.8e-03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKRKR 5
 Db 8 RKGR 12

RESULT 26

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 13, 2006, 08:42:09 ; Search time 227 Seconds
Perfect score: 30 (without alignments)
Sequence: 1 RGRKR 6

Title: US-09-816-688B-1
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 70528306 residues

Total number of hits satisfying chosen parameters: 15779
Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

UniProt 05.80:*

1: uniprot_sprot:
2: uniprot_trembl:
*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

\$

Result

No.

Score

Query

Match

Length

DB

ID

Description

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	1	25	83.3	21	2	Q6LD79_9MURI	Q6ld79 mus p. ary	Q6ld79 mus p. ary
2	2	25	83.3	21	2	Q6LBC9_MOUSE	Q6le9c mus musculus	Q6le9c mus musculus
3	3	22	73.3	16	2	Q9DBH9_XENLA	Q9ud21 homo sapien	Q9ud21 homo sapien
4	4	22	73.3	20	2	Q7M3Z3_ILLAR	Q9d69 xenopus lae	Q9d69 xenopus lae
5	5	22	73.3	21	2	Q5RF91_PONPY	Q7m3z3 illex argen	Q7m3z3 illex argen
6	6	21	70.0	15	2	Q5RF91_PONPY	Q5rf91 pongo pygma	Q5rf91 pongo pygma
7	7	21	70.0	15	2	Q55411_MOUSE	Q35411 mus musculus	Q35411 mus musculus
8	8	21	70.0	17	2	Q76N52_HUMAN	Q76n52 homo sapien	Q76n52 homo sapien
9	9	21	70.0	19	2	Q9UDB7_HUMAN	Q9udb7 homo sapien	Q9udb7 homo sapien
10	10	21	70.0	19	2	Q8T0Y5_APIME	Q8t0y5 apis mellif	Q8t0y5 apis mellif
11	11	21	70.0	20	2	Q9ZG97_9DELA	Q4zg97 human t-lym	Q4zg97 human t-lym
12	12	21	70.0	20	2	Q4ZGB1_9DELA	Q4zgb1 human t-lym	Q4zgb1 human t-lym
13	13	21	70.0	20	2	Q4ZGB2_9DELA	Q4zgb2 human t-lym	Q4zgb2 human t-lym
14	14	21	70.0	21	2	Q9UC26_HUMAN	Q9uc26 homo sapien	Q9uc26 homo sapien
15	15	21	70.0	19	2	Q9IG23_9VIRU	Q9jg23 torque teno	Q9jg23 torque teno
16	16	21	70.0	21	2	Q9IG26_9VIRU	Q9jg26 torque teno	Q9jg26 torque teno
17	17	21	70.0	20	2	Q9IG30_9VIRU	Q4zg97 human t-lym	Q4zg97 human t-lym
18	18	20	66.7	10	2	Q8VN85_HELIPY	Q8vn85 helicobacte	Q8vn85 helicobacte
19	19	20	66.7	14	2	Q4CX76_9CUCU	Q4gx76 turculio gl	Q4gx76 turculio gl
20	20	66.7	19	2	Q8BYW9_BOVIN	Q8hyw9 bos taurus	Q8hyw9 bos taurus	
21	20	66.7	19	2	Q8PU92_BRARE	Q8pu92 brachydanio	Q8pu92 brachydanio	
22	22	66.7	21	2	Q9IG26_9VIRU	Q66mt0 human immun	Q66mt0 human immun	
23	23	66.7	20	2	QAYAE2_PLABB	Q4yae2 plasmodium	Q4yae2 plasmodium	
24	24	66.7	21	1	TKNC_CARAU	P25421 carassius a	P25421 carassius a	
25	25	66.7	21	2	Q7M3M1_HEMPU	Q7m3ml hemirot	Q7m3ml hemirot	
26	26	66.7	21	2	Q6Z2J7_BORGA	Q662j7 borrelia ga	Q662j7 borrelia ga	
27	27	66.7	21	2	Q9PDR39_NIPNI	Q9dd39 nipponia ni	Q9dd39 nipponia ni	
28	28	66.7	21	2	Q9PRZ3_NCMY	Q9prz3 oncorhynchu	Q9prz3 oncorhynchu	
29	29	63.3	10	2	Q7OY78_9LAMI	Q7oy78 plectranthu	Q7oy78 plectranthu	
30	30	63.3	11	2	Q7OY85_9LAMI	Q7oy85 platostra	Q7oy85 platostra	
31	31	63.3	13	2	Q65331_NPVAC	Q65331 autographa	Q65331 autographa	

32	19	63.3	33	2	Q7OY82_9LAMI	Q7oy82 plectranthu	Q7oy82 plectranthu
33	19	63.3	34	2	Q5XPT1_SOLTU	Q5xpt1 solanum tub	Q5xpt1 solanum tub
34	19	63.3	35	2	Q5PX33_9CHLO	Q5px33 9chloro	Q5px33 9chloro
35	19	63.3	35	2	Q7WRZ1_9PLAO	Q7wrz1 flavobacter	Q7wrz1 flavobacter
36	19	63.3	37	2	Q5PX35_9CHLO	Q5px35 halimeda tu	Q5px35 halimeda tu
37	19	63.3	38	2	Q16173_HUMAN	homo sapien	homo sapien
38	19	63.3	39	2	Q9UH46_HUMAN	homo sapien	homo sapien
39	19	63.3	40	2	Q7OY86_9LAMI	Q7oy86 platostra	Q7oy86 platostra
40	19	63.3	41	2	Q7S325_NEUCL	Q7s325 neurospora	Q7s325 neurospora
41	19	63.3	42	2	Q6UQN2_9PASS	Q6uqn2 anomalogiz	Q6uqn2 anomalogiz
42	19	63.3	43	2	Q6UQN3_9PASS	Q6uqn3 vidua orien	Q6uqn3 vidua orien
43	19	63.3	44	2	Q6UQN4_9PASS	Q6uqn4 vidua parad	Q6uqn4 vidua parad
44	19	63.3	45	2	Q6UQN5_9PASS	Q6uqn5 vidua obtus	Q6uqn5 vidua obtus
45	19	63.3	46	2	Q6UQN6_9PASS	Q6uqn6 vidua hypoc	Q6uqn6 vidua hypoc
46	19	63.3	47	2	Q6UQN7_9PASS	Q6uqn7 vidua macro	Q6uqn7 vidua macro
47	19	63.3	48	2	Q6UQN8_9PASS	Q6uqn8 vidua wilso	Q6uqn8 vidua wilso
48	19	63.3	49	2	Q6UQN9_9PASS	Q6uqn9 vidua caner	Q6uqn9 vidua caner
49	19	63.3	50	2	Q6UQP2_9PASS	Q6uqp2 vidua ratic	Q6uqp2 vidua ratic
50	19	63.3	51	2	Q6UQP3_9PASS	Q6uqp3 vidua purpu	Q6uqp3 vidua purpu
51	19	63.3	52	2	Q6UQP4_9PASS	Q6uqp4 vidua regia	Q6uqp4 vidua regia
52	19	63.3	53	2	Q6UQP5_9PASS	Q6uqp5 vidua fitch	Q6uqp5 vidua fitch
53	19	63.3	54	2	Q4XNU6_PLACH	Q4xnu6 plasmodium	Q4xnu6 plasmodium
54	19	60.0	55	2	Q8R2J7_MESAU	Q8r2j7 mesococc	Q8r2j7 mesococc
55	18	60.0	56	2	Q9R8R9_STRPY	Q9r8r9 streptococ	Q9r8r9 streptococ
56	18	60.0	57	2	Q6LC05_PSEAS	Q6lc05 pseudomonas	Q6lc05 pseudomonas
57	18	60.0	58	2	Q7L212_MELGZA	Q7l212 meliagris g	Q7l212 meliagris g
58	18	60.0	59	2	P79167_HORSE	P79167 horse	P79167 horse
59	18	60.0	60	2	Q6KC74_BUCCG	Q6kc74 buccal	Q6kc74 buccal
60	18	60.0	61	2	Q7RNN4_PLATO	Q7rnn4 plasmidum	Q7rnn4 plasmidum
61	18	60.0	62	2	Q4XDU3_PLACH	Q4xdus3 plasmidum	Q4xdus3 plasmidum
62	18	60.0	63	2	Q4Y054_PLACH	Q4y054 plasmidum	Q4y054 plasmidum
63	18	60.0	64	2	Q4Y6H4_PLATIV	Q4y6h4 plasmidum	Q4y6h4 plasmidum
64	18	60.0	65	2	Q90518_9HIV1	Q90518 human immun	Q90518 human immun
65	18	60.0	66	2	Q905J6_9HIV1	Q905j6 human immun	Q905j6 human immun
66	18	60.0	67	2	Q90RF8_9HIV1	Q90rf8 human immun	Q90rf8 human immun
67	18	60.0	68	2	Q9UCM1_HUMAN	Q9ucm1 homo sapien	Q9ucm1 homo sapien
68	18	60.0	69	2	Q7RCK5_PLATO	Q7rck5 plasmidum	Q7rck5 plasmidum
69	18	60.0	70	2	P92210_AGRCR	P92210 agricory c	P92210 agricory c
70	17	56.7	71	2	P92214_9POAL	P92214 ambopyrum	P92214 ambopyrum
71	17	56.7	72	2	P92218_9POAL	P92218 australopyrum	P92218 australopyrum
72	17	56.7	73	2	P92221_BROIN	P92221 bromus iner	P92221 bromus iner
73	17	56.7	74	2	P92226_CRIDS	P92226 crithopis	P92226 crithopis
74	17	56.7	75	2	P92372_HAYNALIA	P92372 haynaldia v	P92372 haynaldia v
75	17	56.7	76	2	P92385_HORMA	P92385 hordeum mar	P92385 hordeum mar
76	17	56.7	77	2	P92387_HEMTRAL	P92387 hemeraria p	P92387 hemeraria p
77	17	56.7	78	2	P92387_HETP1	P92387 heteranthel	P92387 heteranthel
78	17	56.7	79	2	P92393_HORVU	P92393 hordeum vul	P92393 hordeum vul
79	17	56.7	80	2	P92403_LOPHYRUM	P92403 lophyrum	P92403 lophyrum
80	17	56.7	81	2	P92421_PSAFR	P92421 psafra	P92421 psafra
81	17	56.7	82	2	P92425_PSEPI	P92425 psepi	P92425 psepi
82	17	56.7	83	2	P92427_PERDICTYON	P92427 perdictyon	P92427 perdictyon
83	17	56.7	84	2	P92430_AEGILOPS	P92430 aegilops ta	P92430 aegilops ta
84	17	56.7	85	2	P92440_THIBERI	P92440 thiopyrum	P92440 thiopyrum
85	17	56.7	86	2	P92442_TAIBERI	P92442 taeniamathra	P92442 taeniamathra
86	17	56.7	87	2	P92442_TIBERI	P92442 tiberia	P92442 tiberia
87	17	56.7	88	2	P9YI09_ADB04	P9yi09 adb04	P9yi09 adb04
88	17	56.7	89	2	P9YI09_ADE07	P9yi09 ade07	P9yi09 ade07
89	17	56.7	90	2	Q9YVE3_ADB07	Q9yve3 human adeno	Q9yve3 human adeno
90	17	56.7	91	2	P94271_HPV19	P94271 human papil	P94271 human papil
91	17	56.7	92	2	P94273_HPV25	P94273 human papil	P94273 human papil
92	17	56.7	93	2	P94276_NEUCR	P94276 clostridium	P94276 clostridium
93	17	56.7	94	2	P94277_QBFYR0	P94277 buxbaumia a	P94277 buxbaumia a
94	17	56.7	95	2	P9UMB9_HUMAN	P9umb9 human adeno	P9umb9 human adeno
95	17	56.7	96	2	P96F86_SPHAGNUM	P96f86 sphagnum gi	P96f86 sphagnum gi
96	17	56.7	97	2	P96F86_BRVOY	P96f86 brvoym	P96f86 brvoym
97	17	56.7	98	2	P96F89_TAKLIS	P96f89 taklis	P96f89 taklis
98	17	56.7	99	2	P7S9F5_NEUCR	P7s9f5 neurospora	P7s9f5 neurospora
99	17	56.7	100	2	P93M85_SUS	P93m85 sus scrofa	P93m85 sus scrofa
100	17	56.7	101	2	P15344_HUMAN	P15344 human adeno	P15344 human adeno
101	17	56.7	102	2	P9UD45_HUMAN	P9ud45 human adeno	P9ud45 human adeno
102	17	56.7	103	2	P9UD47_HUMAN	P9ud47 human adeno	P9ud47 human adeno
103	17	56.7	104	2	P95RL96_HUMAN	P95rl96 human adeno	P95rl96 human adeno
104	17	56.7	104	2	P94YAA7_PLABE	P94yaa7 plabes	P94yaa7 plabes

RESULT 1									
ID		SEQUENCE		PRT;		PRT;		ALIGNMENTS	
06LD79	9MURI	PRELIMINARY;							
AC	Q6LD79_	9MURI	PRELIMINARY;						
DT	05-JUL-2004	(TREMBrel.	27, Created)						
DT	05-JUL-2004	(TREMBrel.	27, Last sequence update)						
DE	Arylhydrocarbon receptor.								
GN	Name-Ahr;								
OS	Mus sp.								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Murinae; Mus.								
OC	Muridae; Murinae; Mus.								
RN	[1] _								
RP	NUCLEOTIDE SEQUENCE.								
RX	RA Mimura J., Ema M., Sogawa K., Ikawa S., Fujii-Kuriyama Y., "A complete structure of the mouse Ah receptor gene.";								
RA	RT Pharmacogenomics 4:349-354 (1994).								
RL	EMBL; S7644; AAB33978.1; -; Genomic_DNA.								
DR	MGI; MGI:105043; Ahr.								
DR	GO:0004872; F:receptor activity; IEA.								
KW	Receptor.								
SQ	SEQUENCE	21 AA;	2380 MW;	98973F7274F4A65	CRC64;				
RESULT 2									
ID		Q6L8C9_MOUSE PRELIMINARY;		PRT;		21 AA.			
AC		Q6L8C9_		Created)					
DT		05-JUL-2004 (TREMBrel.		27, Last sequence update)					
DT		05-JUL-2004 (TREMBrel.		27, Last annotation update)					
DE		DNA sequence, exon 1 and 5; end of cds. (Fragment).							
GN		Name-Ahr;							
OS		Mus musculus (Mouse).							
OC		OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathus; Muridae; Murinae; Mus.							
NCBI_TaxID=10090;									
RESULT 3									
ID		Q9UD21_HUMAN PRELIMINARY;		PRT;		16 AA.			
AC		Q9UD21_		Created)					
DT		01-MAY-2000 (TREMBrel.		13, Last sequence update)					
DT		01-MAY-2000 (TREMBrel.		13, Last annotation update)					
DE		Cyclin_E_L (Fragment).							
OS		Homo sapiens (Human).							
OC		OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.							
NCBI_TaxID=9606;									
RESULT 4									
ID		Q9UD21_HUMAN PRELIMINARY;		PRT;		16 AA.			
AC		Q9UD21_		Created)					
DT		01-JUN-2000 (TREMBrel.		14, Last sequence update)					
DT		01-JUN-2000 (TREMBrel.		14, Last annotation update)					
DE		Cyclin_E_L (Fragment).							
OS		Homo sapiens (Human).							
OC		OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.							
NCBI_TaxID=9606;									
RESULT 5									
ID		Q9UD21_HUMAN PRELIMINARY;		PRT;		16 AA.			
AC		Q9UD21_		Created)					
DT		01-MAY-2000 (TREMBrel.		13, Last sequence update)					
DT		01-MAY-2000 (TREMBrel.		13, Last annotation update)					
DE		Cyclin_E_L (Fragment).							
OS		Homo sapiens (Human).							
OC		OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.							
NCBI_TaxID=9606;									
RESULT 6									
ID		Q9UD21_HUMAN PRELIMINARY;		PRT;		16 AA.			
AC		Q9UD21_		Created)					
DT		01-JUN-2000 (TREMBrel.		14, Last sequence update)					
DT		01-JUN-2000 (TREMBrel.		14, Last annotation update)					
DE		Cyclin_E_L (Fragment).							
OS		Homo sapiens (Human).							
OC		OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.							
NCBI_TaxID=9606;									
RESULT 7									
ID		Q9UD21_HUMAN PRELIMINARY;		PRT;		16 AA.			
AC		Q9UD21_		Created)					
DT		01-MAY-2000 (TREMBrel.		13, Last sequence update)					
DT		01-MAY-2000 (TREMBrel.		13, Last annotation update)					
DE		Cyclin_E_L (Fragment).							
OS		Homo sapiens (Human).							
OC		OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.							
NCBI_TaxID=9606;									
RESULT 8									
ID		Q9UD21_HUMAN PRELIMINARY;		PRT;		16 AA.			
AC		Q9UD21_		Created)					
DT		01-MAY-2000 (TREMBrel.		13, Last sequence update)					
DT		01-MAY-2000 (TREMBrel.		13, Last annotation update)					
DE		Cyclin_E_L (Fragment).							
OS		Homo sapiens (Human).							
OC		OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.							
NCBI_TaxID=9606;									
RESULT 9									
ID		Q9UD21_HUMAN PRELIMINARY;		PRT;		16 AA.			
AC		Q9UD21_		Created)					
DT		01-MAY-2000 (TREMBrel.		13, Last sequence update)					
DT		01-MAY-2000 (TREMBrel.		13, Last annotation update)					
DE		Cyclin_E_L (Fragment).							
OS		Homo sapiens (Human).							
OC		OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.							

RT transition."; Mol. Cell. Biol. 15:2612-2624 (1995);
 SQ SEQUENCE 16 AA; 2089 MW; 777EFC59C445B29C CRC64;

Query Match 73.3%; Score 22; DB 2; Length 21;
 Best Local Similarity 66.7%; Pred. No. 1.2e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0;
 Gaps 0; GapS 0;

Qy 1 RKRKR 6
 Db 3 RRRRR 8

RESULT 6
 Q5RF91_PONY_PONY PRELIMINARY; PRT; 15 AA.
 ID Q5RF91_PONY PRELIMINARY;
 AC Q5RF91_PONY PRELIMINARY;
 DT 01-FEB-2005 (TREMBLrel. 29, Created)
 DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
 DB Hypothetical protein DKFP2469P021;
 GN Name=DKFP2469P021;
 OS Pongo Pygmaeus (Orangutan).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 Pongo.
 OC NCBI_TAXID=9600;
 RN RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RG The German cDNA Consortium;
 RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Pobo G.,
 RA Han M., Wleemann S.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL:CR857270; CAA89566.1; -; mRNA.
 KW Hypothetical protein;
 SQ SEQUENCE 15 AA; 1788 MW; 530A15F11C204E3A CRC64;

Query Match 70.0%; Score 21; DB 2; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRRKR 6
 Db 8 KRRKQ 12

RESULT 7
 Q35411_MOUSE_PRELIMINARY; PRT; 15 AA.
 ID Q35411_MOUSE_PRELIMINARY;
 AC Q35411_MOUSE_PRELIMINARY;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DB Beta III spectrin (Fragment).
 GN Name=Spnbs;
 OS Mus musculus (Mouse).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10000;

RN RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole embryo;
 RX MEDLINE=98045634; PubMed=9826670; DOI=10.1073/pnas.95.24.14158;

RESULT 5
 Q7M3Z3_IILLAR_PRELIMINARY; PRT; 21 AA.
 ID Q7M3Z3_IILLAR_PRELIMINARY;
 AC Q7M3Z3_IILLAR_PRELIMINARY;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DB Sperm argentinin protein 12-2 (Fragment).
 OS Ilex argentininus (Argentinian squid).
 OC Bukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoelioidea;
 OC Decapodiformes; Oegopsida; Ommastrephidae; Ilex.
 NCBI_TAXID=6628;
 RN RP PROTEIN SEQUENCE.
 RX MEDLINE=90329035; PubMed=2375775;
 RA Osadchuk L.A., Levina N.B., Tellezhinskaya I.N., Khrapunov S.N.,
 RA Berdyahev G.D., Aldanova N.A.;
 RT "Primary structure of main nuclear protein from headleg mollusk Ilex
 RT argentinus and comparison with sperm protein of other animals.";
 RT Bioorg. Khim. 16:448-455 (1990).
 DR PIR: PN0082; PN0082.
 PT NON_TER 1 1
 PT NON_TER 21 21
 SQ SEQUENCE 21 AA; 2931 MW; A9F8D98969174878 CRC64;

Query Match 70.0%; Score 21; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.7e+03;

RESULT 10

Db	ID	NAME	DEFINITION	TYPE	SEQUENCE	RESULT
	10	RSQRKR 15				RESULT 12
	Q4ZGB1_9DELA	9DELA PRELIMINARY;	PRT;	20 AA.		Q9UC26_HUMAN PRELIMINARY;
	Q4ZGB1;					PRT; 21 AA.
	AC					AC Q9UC26;
	DT	13-SEP-2005 (TREMBLrel. 31, Created)				DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
	DT	13-SEP-2005 (TREMBLrel. 31, Last annotation update)				DT 01-JUN-2000 (TREMBLrel. 13, Last annotation update)
	DB	NCBI-TaxID:11908;				DB Stromelysin-3 (Fragment).
	GN	Name=ex;				OS Homo sapiens (Human).
	GN	Human T-lymphotropic virus 1.				OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
	OS	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;				OC NCBI-TaxID:9606;
	OC	Deltaretrovirus.				OX [1];
	OX					PROTEIN SEQUENCE.
	RN	NUCLEOTIDE SEQUENCE.				RX PMID:95265105; PubMed=7746327; DOI=10.1038/375244a0;
	RC	STRAIN=C7 HC;				RA Pei D.; Weiss S.J.;
	RA	Sabouri A. H., Saito M., Tatsumi R., Hanada K., Usuku K., Furukawa Y., Izumo S., Arimura K., Fujisawa J., Farid R., Osame M.;				RT "Furin"-dependent intracellular activation of the human stromelysin-3 zymogen.";
	RT	Functional and Phylogenetic Analysis of Human T-cell Lymphotropic Virus Type 1 (HTLV-1) tax Subtypes.;				RT Nature 375:244-247(1995).
	RT	Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.				SQ SEQUENCE 21 AA; 2300 MW; BB8C224E96D4B9D6 CRC64;
	RL	EMBL: AB211200; BAD99652.1; -; Genomic_DNA.				Query Match Best Local Similarity 70.0%; Score 21; DB 2; Length 21; Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
	DR	NON_TER 20				QY 1 RKRKR 6
	FT	SEQUENCE 20 AA; 2588 MW; CCE8286F1913DEF9 CRC64;				DB 12 RNRQKR 17
	Qy	Query Match Best Local Similarity 66.7%; Score 21; DB 2; Length 20; Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;				RESULT 15
	Q9GJ23	9VIRU PRELIMINARY;				Q9GJ23 9VIRU PRELIMINARY;
	AC					PRT; 21 AA.
	Q9GJ23;					AC Q9GJ23;
	DT	01-OCT-2000 (TREMBLrel. 15, Created)				DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
	DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)				DT 01-OCT-2004 (TREMBLrel. 26, Last annotation update)
	DB	ORF1 (Fragment).				DB ORF1 (Fragment).
	GN	Name=ORF1;				GN Name=ORF1;
	OS	Torque teno virus.				OS Nucleotide sequence.
	OC	Viruses; ssDNA viruses; Anellovirus.				OC PubMed=10799591;
	OX					OX NCBI-TaxID:66887;
	RN					RN [1];
	RP					RP Nucleotide sequence.
	Q9GJ26	9VIRU PRELIMINARY;				Q9GJ26 9VIRU PRELIMINARY;
	AC					PRT; 21 AA.
	Q9GJ26;					AC Q9GJ26;
	DT	13-SEP-2005 (TREMBLrel. 31, Created)				DT 01-OCT-2000 (TREMBLrel. 15, Created)
	DT	13-SEP-2005 (TREMBLrel. 31, Last sequence update)				DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
	DB	Rex (Fragment).				DT 01-OCT-2004 (TREMBLrel. 26, Last annotation update)
	GN	Name=rex;				DB ORF1 (Fragment).
	OS	Human T-lymphotropic virus 1.				GN Name=ORF1;
	OC	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;				OS Nucleotide sequence.
	OC	Deltaretrovirus.				OC PubMed=10799591;
	OX					OX NCBI-TaxID:11908;
	RN					RN [1];
	RP					RP Nucleotide sequence.
	RC	STRAIN=B2 HAM;				RC Nucleotide sequence.
	RA	Sabouri A. H., Saito M., Tatsumi R., Hanada K., Usuku K., Furukawa Y., Izumo S., Arimura K., Fujisawa J., Farid R., Osame M.;				RA Nucleotide sequence.
	RA	Functional and Phylogenetic Analysis of Human T-cell Lymphotropic Virus Type 1 (HTLV-1) tax Subtypes.;				RA DOI=10.1128/JVI.74.11.5161-5167.2000;
	RT	Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.				RA Okamoto H., Ukita M., Nishiawara T., Kishimoto J., Hoshi Y., Mizuo H., Tanaka T., Miyakawa Y., Mayumi M.;
	RL	EMBL: AB211199; BAD99651.1; -; Genomic_DNA.				RT "Circular double-stranded forms of TT virus DNA in the liver.";
	DR	NON_TER 20				RL J. Virol. 74:5161-5167(2000).
	FT	SEQUENCE 20 AA; 2588 MW; CCE8286F1913DEF9 CRC64;				DR EMBL; AB040786; BAA94205.1; -; Genomic_DNA.
	Qy	Query Match Best Local Similarity 66.7%; Score 21; DB 2; Length 20; Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;				FT NON_TER 21 21
	Q9GJ26	9VIRU PRELIMINARY;				FT Sequence 21 AA; 3001 MW; 969c86599D8A344B CRC64;
	AC					Query Match Best Local Similarity 66.7%; Score 21; DB 2; Length 21; Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
	Q9GJ26;					QY 1 RKRKR 6
	DT	01-OCT-2000 (TREMBLrel. 15, Created)				DB 8 RTRRR 13
	DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)				RESULT 16
	DB	ORF1 (Fragment).				Q9GJ26 9VIRU PRELIMINARY;
	GN	Name=ORF1;				PRT; 21 AA.
	OS	Torque teno virus.				AC Q9GJ26;
	OS	Q9UC26_HUMAN				DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
	OS	Q9UC26_HUMAN				DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
	OS	Q9UC26_HUMAN				DB ORF1 (Fragment).
	OS	Q9UC26_HUMAN				GN Name=ORF1;
	OS	Q9UC26_HUMAN				OS Torque teno virus.

OC	Viruses; ssDNA viruses; Anellovirus.	RC	STRAIN=NQ267;
OX	NCBI_TAXID=68887;	RX	MEDLINE=21625040; PubMed=11742075; DOI=10.1073/pnas.251396098;
RN	[1]	RA	Falush D., Krant C., Taylor N.S., Correa P., Fox J.G., Achtmann M.,
RP	NUCLEOTIDE_SEQUENCE.	RA	Suerbaum S.;
	MEDLINE=20261737; PubMed=10799591;	RT	"Recombination and mutation during long-term gastric colonization by Helicobacter pylori: estimates of clock rates, recombination size and minimal age.";
RX	DOI=10.1128/JVI.74.11.5161-5167.2000;	RT	RT
RX	Okamoto H., Urata M., Nishizawa T., Kishimoto J., Hoshi Y., Mizuo H.,	RL	Proc. Natl. Acad. Sci. U.S.A. 98:15056-15061 (2001).
RA	Tanaka T., Miyakawa Y., Mayumi M.; "Circular double-stranded forms of TT virus DNA in the liver.";	DR	EMBL; AJ18322; CAD1229.1; -; Genomic DNA.
RA	J. Virol. 74:5161-5167 (2000).	SQ	SEQUENCE 10 AA; 1329 MW; 81E80240332411 CRC64;
RT	EMBL: AB040782; BAA94202.1; -; Genomic_DNA.		
DR			
FT	NON_TER 1		
FT	NON_TER 21		
SQ	SEQUENCE 21 AA; 2922 MW; 953F86599DBA344B CRC64;		
Qy	1 RKRKRK 6	Query Match	Score 20; DB 2; Length 10;
	8 RTRRRR 13	Best Local Similarity	50.0%; Pred. No. 1.7e+03;
		Matches	3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db		Qy	1 RKRKRK 6
			:
		Db	4 RKGREK 9
			:
		RESULT 19	RESULT 19
		Q4GX76_9CUCU PRELIMINARY;	Q4GX76_9CUCU PRELIMINARY;
		ID	ID
		Q4GX76_9CUCU PRELIMINARY;	Q4GX76_9CUCU PRELIMINARY;
		AC	AC
		13-SEP-2005 (TREMBLrel. 31, Created)	13-SEP-2005 (TREMBLrel. 31, Last sequence update)
		DT	DT
		13-SEP-2005 (TREMBLrel. 31, Last annotation update)	13-SEP-2005 (TREMBLrel. 31, Last annotation update)
		DT	DT
		Ribosomal protein L4le (Fragment).	Ribosomal protein L4le (Fragment).
		GN	GN
		Name-rpL4le;	Name-rpL4le;
		IS	IS
		Circulio glandium.	Circulio glandium.
		OC	OC
		Neoplera; Endopterygota; Coleoptera; Polypaga; Pterygota;	Neoplera; Endopterygota; Coleoptera; Polypaga; Cucujiformia;
		OC	Cucujiformia; Curculionidae; Curculioninae; Curculionini; Curculio.
		OX	OX
		[1] —	[1] —
		NCBI_TaxID=197013;	NCBI_TaxID=197013;
		RN	RN
		NUCLEOTIDE_SEQUENCE.	NUCLEOTIDE_SEQUENCE.
		RA	RA
		Longhorn S.J.; Vogler A.P.;	Longhorn S.J.; Vogler A.P.;
		RT	RT
		"Ribosomal proteins of Coleoptera.";	"Ribosomal proteins of Coleoptera.";
		RL	RL
		Submitted (JUN 2005) to the EMBL/GenBank/DBJ databases.	Submitted (JUN 2005) to the EMBL/GenBank/DBJ databases.
		DR	DR
		EMBL; AM04914; CAJ17447.1; -; mRNA.	EMBL; AM04914; CAJ17447.1; -; mRNA.
		KW	KW
		Ribosomal protein.	Ribosomal protein.
		FT	FT
		NON_TER 14	NON_TER 14
		SQ	SQ
		SEQUENCE 14 AA; 1912 MW; 53EE2A7E350113A33 CRC64;	SEQUENCE 14 AA; 1912 MW; 53EE2A7E350113A33 CRC64;
		Query Match	Query Match
		Score 20; DB 2; Length 14;	Score 20; DB 2; Length 14;
		Best Local Similarity	Best Local Similarity
		66.7%; Pred. No. 2.4e+03;	66.7%; Pred. No. 2.4e+03;
		Matches 4; Conservative 4; Mismatches 1; Indels 1; Gaps 0; Gaps 0;	Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0; Gaps 0;
Qy	1 RKRKRK 6	Qy	1 RKRKRK 6
	8 RTRRRR 13		:
Db		Db	6 RKGREK 11
			:
		RESULT 20	RESULT 20
		Q8HTW9_BOVIN PRELIMINARY;	Q8HTW9_BOVIN PRELIMINARY;
		ID	ID
		Q8HTW9_BOVIN PRELIMINARY;	Q8HTW9_BOVIN PRELIMINARY;
		AC	AC
		01-MAR-2003 (TREMBLrel. 23, Created)	01-MAR-2003 (TREMBLrel. 23, Last sequence update)
		DT	DT
		01-MAR-2003 (TREMBLrel. 23, Last annotation update)	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
		DT	DT
		Calcium channel alpha-2/delta subunit 1 (Fragment).	Calcium channel alpha-2/delta subunit 1 (Fragment).
		DB	DB
		Bos taurinus (Bovine).	Bos taurinus (Bovine).
		OS	OS
		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		OC	OC
		Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
		OC	OC
		Pecora; Bovidae; Bovinae; Bos.	Pecora; Bovidae; Bovinae; Bos.
		NCBI_TaxID=9913;	NCBI_TaxID=9913;
		RN	RN
		NUCLEOTIDE_SEQUENCE.	NUCLEOTIDE_SEQUENCE.
		RC	RC
		STRAIN=Hostein-Prisian; TISSUE=Leukocyte;	STRAIN=Hostein-Prisian; TISSUE=Leukocyte;
		RA	RA
		Buitkamp J.;	Buitkamp J.;
		RL	RL
		Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
		DR	DR
		[1]	[1]
		NUCLEOTIDE_SEQUENCE.	NUCLEOTIDE_SEQUENCE.
		OC	OC
		Helicobacteraceae; Helicobacter.	Helicobacteraceae; Helicobacter.
		OX	OX
		RN	RN
		[1]	[1]
		NUCLEOTIDE_SEQUENCE.	NUCLEOTIDE_SEQUENCE.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC PIR: JH0361; JH0361.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PFAM; PF02202; Tachykinin_1.
 DR PROSITE; PS00267; "TACHYKININ_1.
 Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.
 KW MOD_RES 21 AA; 2369 MW; 1460DC6C5B097A29 CRC64;
 SQ SEQUENCE 21 AA; 2369 MW; 1460DC6C5B097A29 CRC64;

Query Match 66.7%; Score 20; DB 1; Length 21;
 Best Local Similarity 80.0%; Pred. No. 3.6e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; MisMatches 1; Indels 1; Gaps 0;

Qy 1 RKRKRK 5
 Db 9 RKRHK 13

RESULT 25
 ID Q7M4M1_HEMPU PRELIMINARY;
 AC Q7M4M1;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Histone H1 (Fragment).
 OS Hemicentrotus pulcherrimus (Sea urchin).
 OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
 OC Hemicentrotus.
 RN [1] -
 RP PROTEIN SEQUENCE.
 RX MEDLINE=91115778; PubMed=2126010;
 RA Suzuki M.; Sugura M.; Ebashi S.;
 RT "Sea urchin protease specific to the SPKK motif in histone.";
 RL J. Biochem. 108:347-355 (1990).
 DR PIR; PS0146; PS0146.
 FT NON-TER 1
 FT NON-TER 21 21
 SQ SEQUENCE 21 AA; 2378 MW; 0B32BA52DD06D7 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 21;
 Best Local Similarity 80.0%; Pred. No. 3.6e+03; Mismatches 0; Indels 1; Gaps 0;
 Matches 4; Conservative 0; MisMatches 1; Indels 1; Gaps 0;

Qy 1 RKRKRK 5
 Db 13 RSRRK 17

RESULT 26
 ID Q66237_BORG_A PRELIMINARY;
 AC Q66237;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DB Hypothetical protein.
 GN OrderedLocusNames=3801666;
 OS Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
 OC Borrelia burgdorferi group.
 QX NCBI_TaxID=29519;
 [1]

RP NUCLEOTIDE SEQUENCE.
 STRAIN=Pbi;
 RC Gschneidner G.; Lehmann R.; Romualdi A.; Pradella S.;
 RA Schulte-Schreel U.; Wilcke B.; Suenkel J.; Platzter M.;
 RT "Comparative analysis of the *Borrelia garinii* genome.";
 RL Submitted (JUN-2004); AAU07024; 1; -; Genomic DNA.
 DR EMBL; CP000013; AAU07024; 1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 21 AA; 2526 MW; 7FC4CC18506B3D3 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 21;
 Best Local Similarity 50.0%; Pred. No. 3.6e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 3; Conservative 3; MisMatches 0; Indels 0;

Qy 1 RKRKRK 6
 Db 10 QKKEKEK 15

RESULT 27
 ID Q9DD39_NIPNI PRELIMINARY;
 AC Q9DD39;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-PFB-2005 (TREMBLrel. 29, Last annotation update)
 DB Non-W-chromodomain helicase DNA binding protein (W-linked chromodomain
 DE helicase DNA binding protein) (Fragment).
 GN Name-non-W CHD; Synonyms=W-linked CHD;
 OS Nipponia nippon (Crested ibis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Ciconiiformes; Threskiornithidae;
 OC Nipponia.
 RN [1] - TaxID=128390;

RP NUCLEOTIDE SEQUENCE.
 RA Arai Y.; Ishii S.; Kikuchi M.;
 RL Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB019441; BAB15805.1; -; Genomic DNA.
 DR AB019441; BAB15804.1; -; Genomic DNA.
 DR GO:0004386; F:helicase activity; IEA.
 DR GO:0004386; F:helicase activity; IEA.

QX NCBI_TaxID=8022;

Query Match 66.7%; Score 20; DB 2; Length 21;
 Best Local Similarity 66.7%; Pred. No. 3.6e+03; Mismatches 1; Indels 0; Gaps 0;
 Matches 4; Conservative 4; MisMatches 1; Indels 1; Gaps 0;

Qy 1 RKRKRK 6
 Db 4 RKRICK 9

RESULT 28
 ID Q9PR23_ONCAY PRELIMINARY;
 AC Q9PR23;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DB Neuropeptide-gamma (NP-gamma) (Tachykinin homolog).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 RN [1] -
 RP PROTEIN SEQUENCE.
 RX MEDLINE=94056590; PubMed=7694488;
 RA Jensen J.; Olson K.R.; Conlon J.M.;
 RT "Primary structures and effects on gastrointestinal motility of

OC lanids; Lamiaceae; Nepetoideae; Ocimeae; Platostoma.

RT tachykinins from the rainbow trout.";

RL Am. J. Physiol. 265:R804-R810 (1993).

DR GO: 0005102 P: receptor binding; IEA.

GO: GO:0007218 P: neuropeptide signaling pathway; IEA.

DR GO: GO:0007268 P: synaptic transmission; IEA.

DR GO: GO:0007217 P: tachykinin signaling pathway; IEA.

DR Intero. IPR00040 P: tachykinin signaling pathway; IEA.

DR PF02022 P: tachykinin 1.

DR PROSITE: PS00267 Tachykinin 1; UNKNOWN_1.

KW Neuropeptide; Tachykinin.

SEQUENCE 21 AA; 2385 MW; 080CAC636997A29 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 21;

Best Local Similarity 80.0%; Pred. No. 3.6e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKRKRK 5

Db 9 RKRHK 13

RESULT 29

Q70Y78 9LAMI

ID Q70Y78_9LAMI PRELIMINARY; PRT; 10 AA.

AC Q70Y78;

DT 05-JUL-2004 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DR Ribosomal protein (Fragment).

GN Name=rpB16;

OS Plectranthus parishii.

OC Chloroplast.

OC Burkaria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;

OC lamiids; Lamiaceae; Nepetoideae; Ocimeae; Plectranthus.

NCBI_TaxID=204190;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX PubMed=15019625; DOI=10.1016/j.ymprev.2003.08.002;

RA Paton A., Springate D.A., Sudde S., Otiemo D., Grayer R., Harley M.M., Willis F., Simonds M.S.J., Powell M.P., Savolainen V.,

RA "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)"

RT based on three plastid DNA regions";

RL Mol. Phylogenet. Evol. 31:277-299 (2004).

EMBL; AJ505390; CAD4510.1; -; Genomic DNA.

DR GO: GO:0003735 P: structural constituent of ribosome; IEA.

KW Ribosomal protein.

FT NON TER 1 1

FT NON TER 10 10

SQ SEQUENCE 10 AA; 1299 MW; 87C8C86723241411 CRC64;

Query Match 63.3%; Score 19; DB 2; Length 10;

Best Local Similarity 80.0%; Pred. No. 2.6e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKRKRK 5

Db 2 RTRRK 6

RESULT 30

Q70Y75 9LAMI

ID Q70Y75_9LAMI PRELIMINARY; PRT; 11 AA.

AC Q70Y75;

DT 05-JUL-2004 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DR Ribosomal protein (Fragment).

GN Name=rpB16;

OS Platostoma rubrum.

OC Chloroplast.

OC Burkaria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;

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